METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES, METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME

Field of the Invention

The present invention provides a method for obtaining thermostable enzymes. The present invention also provides variants of DNA polymerase I from *Thermus aquaticus*. The present invention further provides methods of identifying mutant DNA polymerases having enhanced catalytic activity. The present invention also provides polynucleotides, expression systems, and host cells encoding the mutant DNA polymerases. Still further, the present invention provides a method to carry out reverse transcriptase-polymerase chain reaction (RT-PCR) and kits to facilitate the same.

Discussion of the Background

Filamentous phage display is commonly used as a method to establish a link between a protein expressed as a fusion with a phage coat protein and its corresponding gene located within the phage particle (Marks et al., 1992). The use of filamentous phage particles as a chemical reagent provides further a strategy to create a complex between an enzyme, its gene and a substrate (Jestin et al., 1999). This substrate can be cross-linked on the surface of filamentous phage using the nucleophilic properties of coat proteins. If the enzyme is active, conversion of the substrate to the product yields a phage particle cross-linked with the product, which can be captured by affinity chromatography (Jestin et al., 1999).

Several similar approaches based on product formation for the isolation of genes encoding enzymes using phage display have been described in the literature for various enzymes (Fastrez et al., 2002). These *in vitro* selections of proteins for catalytic activity are well suited for use with large repertoires of about 10^8 proteins or more. Several libraries of enzyme variants on phage have been constructed and catalytically active proteins with wild type like activities have been isolated (Atwell & Wells, 1999; Heinis et al., 2001; Ponsard et al., 2001; Ting et al., 2001). Mutants with different substrate specificities have been also obtained (Xia et al., 2002). In these studies, the fraction of

active variants in the libraries can be large and it remains unclear how rare an enzyme can be in the initial protein library so as to be selected after iterative selection cycles. Accordingly, there remains a critical need for an efficient process for making and identifying thermostable enzymes possessing a desired catalytic activity (see discussion in Vichier-Guerre & Jestin, 2003).

Reverse transcriptases are enzymes that are present generally in certain animal viruses (i.e., retroviruses), which are used *in vitro* to make complementary DNA (cDNA) from an mRNA template. Practically, reverse transcriptases have engendered significant interest for their use in reverse transcriptase-polymerase chain reaction (RT-PCR). As such, these proteins lend themselves to be a model system for development of an efficient method of making thermostable enzymes having a desired activity.

RNA generally contains secondary structures and complex tertiary sections, accordingly it is highly desired that the RNA be copied in its entirety by reverse transcription to ensure that integrity of cDNA is maintained with high accuracy. However, due to the often complicated secondary and tertiary structures of RNA, the denaturation temperatures are generally about 90°C and, as such, the reverse transcriptase must be capable of withstanding these extreme conditions while maintaining catalytic efficiency.

The classically utilized enzymes for RT-PCR have been isolated from the AMV (Avian myeloblastosis virus) or MMLV (Moloney murine leukemia virus); however, these enzymes suffer from a critical limitation in that they are not thermostable. In fact, the maximum temperature tolerated by most commercially available reverse transcriptases is about 70°C.

One common approach to overcome this limitation in the existing technology with the previously described polymerases has been the use of a protein chaperones in addition to the polymerase. However, this method leads to problems associated with environmental compatibility metal ion requirements, multi-stage procedures, and overall inconvenience. Accordingly, an alternative strategy has been to use thermostable reverse transcriptases. This approach makes it possible to perform multiple denaturation and reverse transcription cycles using only a single enzyme.

To this end, the DNA-dependent DNA polymerase I of *Thermus aquaticus* (i.e., Taq polymerase), is thermostable and has reverse transcriptase activity only in the

presence of manganese. However, when the manganese ion concentration is maintained in the millimolar range the fidelity of the enzyme is affected. It has been suggested that the thermostable DNA-dependent DNA polymerase of *Bacillus stearothermophilus* has reverse transcriptase activity, even in absence of magnesium, but in this case it is necessary to add a thermostable DNA polymerase for the PCR.

Therefore, there remains a critical need for high efficiency, thermostable enzymes that are capable of catalyzing reverse transcription and subsequent DNA polymerization in "one-pot" RT-PCR. Accordingly, the present invention provides an isolated population of thermostable reverse transcriptases, which are active in absence of manganese, by directed evolution of the Stoffel fragment of the Taq polymerase.

SUMMARY OF THE INVENTION

It is an object of the present invention to provide a method of identifying thermostable mutant polypeptides having a catalytic activity by:

a) packaging a vector in which a gene or fragment thereof encoding variants of a catalytic domain responsible for the catalytic activity fused to a gene encoding a phage coat protein;

b) isolation and purification of phage particles;

c) heating the phage-mutant polypeptide at a temperature ranging from 50°C to 90°C for a time ranging from less than 1 minute to several hours;

d) cross-linking a specific substrate with a phage particle;

e) forming a reaction product from the substrate catalyzed by the thermostable mutant protein on phage, wherein the temperature is optionally regulated to be the same or greater or lower than the temperature of (c);

f) selecting the phage particles comprising a variant nucleotidic sequence encoding for the catalytic domain responsible for the catalytic activity at the regulated temperature, by capturing the reaction product or screening for said reaction product;

g) infecting *E. coli* with the phage particles selected at step (f);

h) incubating the infected *E. coli*; and

i) assessing catalytic activity of the proteins corresponding to isolated genes.

It is an object of the present invention to provide a thermostable mutant DNA polymerase having at least 80% homology, preferably at least 90%, more preferably at

least 95%, most preferably at least 97.5%, to the Stoffel fragment of DNA polymerase I obtained from *Thermus aquaticus* (residues 13-555 of SEQ ID NO: 26, which correspond to residues 290-832 of the wild-type DNA polymerase I from *Thermus aquaticus* (SEQ ID NO: 100)).

To this end, the present invention provides thermostable polypeptides having at least 80% homology, preferably at least 90%, more preferably at least 95%, most preferably at least 97.5%, to residues 13-555 of SEQ ID NO: 26, wherein said polypeptide has at least one mutation selected from the group consisting of a mutation in amino acids 461-490 of SEQ ID NO:26 (738 to 767 of the Taq polymerase wild-type sequence SEQ ID NO: 100), A331T (position 608 of the Taq polymerase wild-type sequence SEQ ID NO: 100), S335N (position 612 of the Taq polymerase wild-type sequence SEQ ID NO: 100), M470K (position 747 of the Taq polymerase wild-type sequence SEQ ID NO: 100), M470R (position 747 of the Taq polymerase wild-type sequence SEQ ID NO: 100), F472Y (position 749 of the Taq polymerase wild-type sequence SEQ ID NO: 100), M484V (position 761 of the Taq polymerase wild-type sequence SEQ ID NO: 100), M484T (position 761 of the Taq polymerase wild-type sequence SEQ ID NO: 100), and W550R (position 827 of the Taq polymerase wild-type sequence SEQ ID NO: 100), and wherein said polypeptide has improved DNA polymerase activity and retains 5'-3' exonuclease activity. In an object of the present invention, the 3'-5' exonuclease activity of the mutant polypeptide is inactive.

In an object of the present invention, the thermostable mutant DNA polymerase also has a mutation at one or more position selected from A331, L332, D333, Y334, and S335 of SEQ ID NO: 26 (positions 608-612 of the Taq polymerase wild-type sequence SEQ ID NO: 100).

Therefore, in an object of the present invention, the thermostable mutant DNA polymerase has at least 80% identity to residues 13-555 of SEQ ID NO: 26 and has a mutation at one or more position selected from H203, F205, T232, E253, Q257, D274, L275, I276, V309, I322, A331, L332, D333, Y334, S335, I361, R374, A384, T387, Y419, P493, M498, G499, M502, L503, V506, R518, A523, A526, P539, E543, and W550 of SEQ ID NO: 26. The present invention also embraces polynucleotides encoding the same.

The present invention also provides thermostable polypeptides having at least 80% homology, preferably at least 90%, more preferably at least 95%, most preferably at least 97.5%, to residues 13-555 of SEQ ID NO: 26, wherein said polypeptide has at least one mutation selected from the group consisting of H203R (position 480 of the Taq polymerase wild-type sequence SEQ ID NO: 100), F205L (position 482 of the Taq polymerase wild-type sequence SEQ ID NO: 100), T232S (position 509 of the Taq polymerase wild-type sequence SEQ ID NO: 100), E253G (position 530 of the Taq polymerase wild-type sequence SEQ ID NO: 100), Q257R (position 534 of the Taq polymerase wild-type sequence SEQ ID NO: 100), D274G (position 551 of the Taq polymerase wild-type sequence SEQ ID NO: 100), L275H (position 552 of the Taq polymerase wild-type sequence SEQ ID NO: 100), L275P (position 552 of the Taq polymerase wild-type sequence SEQ ID NO: 100), I276F (position 553 of the Taq polymerase wild-type sequence SEQ ID NO: 100), V309I (position 586 of the Taq polymerase wild-type sequence SEQ ID NO: 100), I322N (position 599 of the Taq polymerase wild-type sequence SEQ ID NO: 100), A331V (position 608 of the Taq polymerase wild-type sequence SEQ ID NO: 100), S335N (position 612 of the Taq polymerase wild-type sequence SEQ ID NO: 100), I361F (position 638 of the Taq polymerase wild-type sequence SEQ ID NO: 100), R374Q (position 651 of the Taq polymerase wild-type sequence SEQ ID NO: 100), A384T (position 661 of the Taq polymerase wild-type sequence SEQ ID NO: 100), T387A (position 664 of the Taq polymerase wild-type sequence SEQ ID NO: 100), Y419C (position 696 of the Taq polymerase wild-type sequence SEQ ID NO: 100), Y419N (position 696 of the Taq polymerase wild-type sequence SEQ ID NO: 100), E465K (position 742 of the Taq polymerase wild-type sequence SEQ ID NO: 100), M470K (position 747 of the Taq polymerase wild-type sequence SEQ ID NO: 100), M470R (position 747 of the Taq polymerase wild-type sequence SEQ ID NO: 100), F472Y (position 749 of the Taq polymerase wild-type sequence SEQ ID NO: 100), F472S (position 749 of the Taq polymerase wild-type sequence SEQ ID NO: 100), A487T (position 764 of the Taq polymerase wild-type sequence SEQ ID NO: 100), K490E (position 767 of the Taq polymerase wild-type sequence SEQ ID NO: 100), P493T (position 770 of the Taq polymerase wild-type sequence SEQ ID NO: 100), M498T (position 775 of the Taq polymerase wild-type sequence SEQ ID NO: 100), G499E (position 776 of the Taq

polymerase wild-type sequence SEQ ID NO: 100), M502K (position 779 of the Taq polymerase wild-type sequence SEQ ID NO: 100), L503P (position 780 of the Taq polymerase wild-type sequence SEQ ID NO: 100), V506I (position 783 of the Taq polymerase wild-type sequence SEQ ID NO: 100), A523V (position 800 of the Taq polymerase wild-type sequence SEQ ID NO: 100), A526V (position 803 of the Taq polymerase wild-type sequence SEQ ID NO: 100), P539S (position 816 of the Taq polymerase wild-type sequence SEQ ID NO: 100), E543K (position 820 of the Taq polymerase wild-type sequence SEQ ID NO: 100), and W550R (position 827 of the Taq polymerase wild-type sequence SEQ ID NO: 100), and wherein said polypeptide has improved DNA polymerase activity and retains 5'-3' exonuclease activity. In an object of the present invention, the 3'-5' exonuclease activity of the mutant polypeptide is inactive.

In a particular object of the present invention, the mutant DNA polymerase has a sequence corresponding to residues 13-555 of one of the following sequences: SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, and SEQ ID NO: 38.

In another object of the present invention, the mutant DNA polymerase has a sequence corresponding to residues 1-543 of one of the following sequences: SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, and SEQ ID NO: 99. Further, in another object of the present invention are polynucleotides that encode for the aforementioned thermostable mutant DNA polymerases.

In yet another object of the present invention is a kit for DNA amplification, which contains: (a) one or more of the aforementioned thermostable mutant DNA polymerases; (b) a concentrated buffer solution, wherein when said concentrated buffer is admixed with the isolated polypeptide the overall buffer concentration is 1X; (c) one or more divalent metal ion (e.g., Mg^{2+} or Mn^{2+}); and (d) deoxyribonucleotides.

In yet another object of the present invention is a method of reverse transcribing RNA by utilizing the inventive thermostable mutant DNA polymerases.

In still a further object of the present invention is a phage-display method for identifying thermostable mutant DNA polymerases in which the Stoffel fragment has been mutated, while the DNA polymerase activity and 5'-3' exonuclease activity has been maintained and/or enhanced.

The above objects highlight certain aspects of the invention. Additional objects, aspects and embodiments of the invention are found in the following detailed description of the invention.

BRIEF DESCRIPTION OF THE FIGURES

A more complete appreciation of the invention and many of the attendant advantages thereof will be readily obtained as the same becomes better understood by reference to the following Figures in conjunction with the detailed description below. In the following legends, polymerase **e** corresponds to SEQ ID NO: 26 containing a R518G mutation (see Examples).

Figure 1 shows the reverse transcriptase activity of phage-polymerases assessed as obtained after different rounds of selection in the presence of Mg^{2+} or Mn^{2+} ions. The lane labels correspond to the following:

MnCl2	$MgCl_2$
a : phage-polymerases of round 6	h : phage-polymerases of round 6
b : phage-polymerases of round 5	i : phage-polymerases of round 5
c : phage-polymerases of round 4	j : phage-polymerases of round 4
d : phage-polymerases of round 3	k : phage-polymerases of round 3
e : phage-polymerases of round 2	l : phage-polymerases of round 2
f : phage-polymerases of round 1	m : phage-polymerases of round 1
g : phage-polymerases of initial population	n : phage-polymerases of initial population

Figure 2 shows the reverse transcriptase activity of phage-polymerases assessed as obtained after different rounds of selection in the presence of Mg^{2+} ions. The lane designations in Figure 2 are as follows:

Phage-polymerase preheated at 65 °C for 5 min.	Phage-polymerase not preheated
a : phage-polymerases of initial population	h : phage-polymerases of initial population
b : phage-polymerases of round 1	i : phage-polymerases of round 1
c : phage-polymerases of round 2	j : phage-polymerases of round 2
d : phage-polymerases of round 3	k : phage-polymerases of round 3
e : phage-polymerases of round 4	l : phage-polymerases of round 4
f : phage-polymerases of round 5	m : phage-polymerases of round 5
g : phage-polymerases of round 6	n : phage-polymerases of round 6
	o : control AMV-RT, 1 U
	p : control AMV-RT, 0.1 U
	q : control AMV-RT, 0.01 U
	r : control AMV-RT, 0.001 U

Figure 3 shows the reverse transcriptase activity of various monoclonal phage-polymerases obtained after round 6 in the presence of Mg^{2+} ions. The lane designations in Figure 3 are as follows: s = SEQ ID NO: 38; a = SEQ ID NO: 20; d = SEQ ID NO: 24; g = SEQ ID NO: 28; C = AMV-RT; i = SEQ ID NO: 30; m = SEQ ID NO: 32; n = SEQ ID NO: 34; b = SEQ ID NO: 22; and q = SEQ ID NO: 36.

Figure 4 shows the reverse transcriptase activities and the polymerase activities of monoclonal phage-polymerases obtained after the round 6 in the presence of Mg^{2+} or Mn^{2+} ions. The lane designations in Figure 4 are as follows: a = SEQ ID NO: 20; b = SEQ ID NO: 22; d = SEQ ID NO: 24; and e = SEQ ID NO: 26 (containing an R518G mutation).

Figure 5 shows purified mutant polymerases **a**, **b**, and **d** used in polymerase chain reaction. The lanes in the gel appearing in Figure 5 include the three clones corresponding to clones a, b and d on Figure 4. In addition, the positive control was performed using the Stoffel fragment polymerase **e** and the polymerase AMV-RT (Promega). The lanes in Figure 5 are as follows:

lane 1 : : molecular weight marker: PhiX phage DNA digested by *Hae*III
lane 2 : control AMV-RT
lane 3 : b = SEQ ID NO: 22
lane 4 : a = SEQ ID NO: 20
lane 5: e = SEQ ID NO: 26 (containing an R5 18G mutation)
lane 6 : d = SEQ ID NO: 24

Figure 6 shows the purification control of proteins after Co^{+2} affinity chromatography.

Variant a

Well 1 = 8µl Fraction 1
Well 2 = 8µl Fraction 2
Well 3 = 8µl Fraction 3
Well 4 = 8µl Fractions 1+2+3 pooled and concentrated on Ultra Amicon 4 column (Millipore).
OD (**a**) = 0.869 mg/ml.

Variant d

Well 1 = 8µl Fraction 1
Well 2 = 8µl Fraction 2
Well 3 = 8µl Fraction 3
Well 4 = 8µl Fractions 1+2+3 pooled and concentrated on Ultra Amicon 4 column (Millipore).
OD (**d**) = 0.908 mg/ml.

Variant e

Well 1 = 8µl Fraction 1
Well 2 = 8µl Fraction 2
Well 3 = 8µl Fraction 3
Well 4 = 8µl Fractions 1+2+3 pooled and concentrated on Ultra Amicon 4 column (Millipore).
OD (**e**) = 0.958 mg/ml.

Variant b

Well 1 = 8µl Fraction 1
Well 2 = 8µl Fraction 2
Well 3 = 8µl Fraction 3
Well 4 = 8µl Fractions 1+2+3 pooled and concentrated on Ultra Amicon 4 column (Millipore).
OD (**b**) = 0.514 mg/ml.

M is the low range SDS PAGE molecular weight standards. Low Range (BIO-RAD, Ref. 161-0304). Bands located at 97.4 kDa; 66.2 kDa; 45 kDa; 31 kDa; 21 kDa and 14.4 kDa.

Figure 7 shows protein **e** purification by Co^{2+} affinity chromatography followed by heparin affinity chromatography.

Lanes 1 and 2 correspond to the protein **e** after purification by affinity chromatography on a Co^{2+} column. Lanes t1, t2, t3, t4 corresponds to the most concentrated fractions after the two-step purification by affinity chromatography, first on a Co^{2+} column and second on a heparin column. M is the low range SDS PAGE molecular weight standards (Biorad).

Figure 8 shows 20% Polyacrylamide gels electrophoresis obtained with variants **e, a, d** and **b** for the test of primer extension.

Figure 9 shows products of PCR with polymerase **e** and variant **a** as shown by agarose gel after electrophoresis. M is the marker Smartladder (Eurogentec).

Figure 10 shows the results of a PCR reaction using variant **a**. Results shown on a 2% agarose gel: deposit of 15µl of amplification product.

Product of amplification = 475bp.

1. SmartLadder 100bp (EUROGENTEC, *Ref. MW- 1800-02,200 lanes, Small fragment*)
2. Variant **a** MJ Research
3. Variant **a** / MJ Research
4. SmartLadder 100bp
5. Variant **a** / Applied BioSystems
6. Variant **a** / Applied BioSystems

Figure 11 shows Product of RT PCR "one pot" with variant **a.** As shown in the agarose gel after electrophoresis, M is the marker of phage PhiX DNA digested by the restriction enzyme *Hae*III.

Figure 12 shows the reverse transcriptase activity of various monoclonal phage-polymerases obtained after round 6 in the presence of Mg^{2+} ions. The lane designations in Figure 12 are as follows: rt1 = SEQ ID NO: 63; rt2 = SEQ ID NO: 65; rt3 = SEQ ID NO: 67; rt16= SEQ ID NO: 69; rt18 = SEQ ID NO: 71; rt25 = SEQ ID NO: 73; rt26 = SEQ ID NO: 75; rt28 = SEQ ID NO: 77; rt30 = SEQ ID NO: 79; rt31 = SEQ ID NO: 81; rt33 = SEQ ID NO: 83; rt36 = SEQ ID NO: 85; rt43 = SEQ ID NO: 87; rt59 = SEQ ID NO: 89; rt64 = SEQ ID NO: 91; rt70 = SEQ ID NO: 93; rt78 = SEQ ID NO: 95; rt80 = SEQ ID NO: 97; rt86 = SEQ ID NO: 99; and nd = not described here.

DETAILED DESCRIPTION OF THE INVENTION

Unless specifically defined, all technical and scientific terms used herein have the same meaning as commonly understood by a skilled artisan in enzymology, biochemistry, cellular biology, molecular biology, and the medical sciences.

All methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, with suitable methods and materials being described herein. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In case of conflict, the present specification, including definitions, will control. Further, the materials, methods, and examples are illustrative only and are not intended to be limiting, unless otherwise specified.

The present invention provides a method of identifying thermostable mutant polypeptides having a catalytic activity comprising:

a) packaging a vector in which a gene or fragment thereof encoding variants of a catalytic domain responsible for the catalytic activity fused to a gene encoding a phage coat protein;

b) isolation and purification of phage particles;

c) heating the phage-mutant polypeptide at a temperature ranging from 50°C to 90°C, preferably from 55°C to 65°C, more preferably at 65°C for a time ranging from 30 seconds to several hours, preferably from 1 minute to 3 hours, more preferably from 5 minutes to 2 hours, most preferably 10 minutes to 1 hour;

d) cross-linking a specific substrate with a phage particle;

e) forming a reaction product from the substrate catalyzed by the thermostable mutant polypeptide on phage, wherein the temperature is optionally regulated to be the same or greater or lower than the temperature of (c) (i.e., from 25°C to 70°C, preferably from 37°C to 70°C and more preferably at 65°C);

f) selecting the phage particles comprising a variant nucleotidic sequence encoding for the catalytic domain responsible for the catalytic activity at the regulated temperature, by capturing the reaction product or screening for said reaction product;

g) infecting *E. coli* with phage particles selected at (f);

h) incubating the infected *E. coli*; and

i) assessing catalytic activity of the proteins corresponding to isolated genes.

In the embodiment above, the gene or fragment thereof encoding variants of a catalytic domain may be directly or indirectly fused to the gene encoding a phage coat protein. When the gene or fragment thereof encoding variants of a catalytic domain and the gene encoding a phage coat protein are indirectly fused it is preferred that the fusion be through a peptide or polypeptide linker.

Within this above-recited embodiment, steps (a) to (h) may be repeated 0 to 20 times, preferably 1 to 15 times, more preferably 2 to 10 times, most preferably 3 to 7 times.

The method comprising a single cycle (repeated 0 times) is particularly adapted to high throughput screening, when steps are repeated from 3 to 7 times, the method is better adapted for classical empirical screening.

The peptide utilized within this embodiment is selected from the group consisting of: a flexible linker such as a glycine rich linker such as $(SG_4)n$ or the sequence SG_4CG_4 (residues 3-12 of SEQ ID NO: 39),

human calmodulin (SEQ ID NO: 46, the DNA encoding SEQ ID NO: 46 is SEQ ID NO: 56), and

hexahistidine binding single chain variable fragment (Grütter M.G., 2002) consisting of:

(i) Anti-His Tag Antibody 3D5 Variable Heavy Chain (SEQ ID NO: 47)

(ii) Linker (SEQ ID NO: 48)

(iii) Anti-His Tag Antibody 3D5 Variable Light Chain (SEQ ID NO: 49).

Moreover, the polypeptide linker is selected from the group consisting of: any protein binding the substrate at high temperature, any catalytic domain such as 5' to 3' exonuclease (from *Thermus thermophilus*, SEQ ID NO: 50), or 3' to 5'exonuclease (from *E. coli*, SEQ ID NO: 51), Catalytic domain of *Bacillus circulans* cyclodextringlycosyltransferase (SEQ ID NO: 52, the DNA is in SEQ ID NO: 57), Catalytic domain of *Bordetella pertussis* adenylate cyclase (SEQ ID NO: 53-the DNA is in SEQ ID NO: 58), *Bacillus amyloliquefaciens* serine protease subtilisin (SEQ ID NO: 54-the DNA is in SEQ ID NO: 59), and Catalytic domain of *Bacillus subtilis* lipase A (SEQ ID NO: 55, Quax W.J., 2003).

As used in the present invention, the cross-linking between the specific substrate of the catalytic domain of the polypeptide with the phage particle is made by a cross-linking agent selected from the group consisting of a: maleimidyl group, iodoacetyl group, disulfide derivative and any other thermostable link (conducting to a stable protein-protein interaction or protein-molecule interaction).

In a preferred embodiment, the catalytic domain may be the catalytic domain of an enzyme selected from the group consisting of: a polymerase, an alpha-amylase (substrate such as starch), a lipase (substrate such as ester), a protease (modified or not modified peptide or polypeptide as substrate), a cyclodextringlycosyltransferase, and an adenylate cyclase.

In another embodiment, the assessment of the catalytic activity of step (f) is made by means of a DNA polymerization.

In yet another embodiment of the present invention, step (b) may be performed after (e) of cross-linking or during (h) of assesing catalytic activity.

As a general method for the isolation of thermostable enzymes and their genes the following should be noted:

First, the gene encoding variants of a catalytic domain are fused to the gene encoding a phage coat protein (such as filamentous phage g3, g6, g7, g9 or g8 protein or of other phage/virus particles) either directly or using a peptide or polypeptide linker such as a short peptide sequence or a protein or a protein domain. These genes encoding phage coat proteins may be fused either at the 3' or at the 5' terminus depending on whether the N- or the C-termini of the proteins are located on the outside of the particle.

This is done either using a phage vector or a phagemid vector used with a helper phage.

Second, the phage-variant enzymes may be heated at a preferred temperature of 65°C for 1 minute or for several hours as appropriate. This step can be performed before or after the substrate cross-linking (maleimidyl group derivatised substrate (DNA primer) crosslinked to the phage particle) and catalysis (DNA polymerisation) steps. Catalysis is preferably at 65°C for 2 minutes, but can be done at any temperature between 0°C and 100°C. Crosslinking is typically performed for 2 hours at 37°C, but can be done at other temperatures (higher temperature may increase maleimidyl hydrolysis versus maleimidyl phage cross-linking).

It is worth noting that the link between the gene and the corresponding enzyme variants is unaltered by high temperatures and the phage particle are still infective and the genes selected can be amplified by *E. coli* after infection (cf. for example, Kristensen P, Winter G., 1998).

By way of example of the aforementioned embodiments, the present invention relates to a purified, thermostable DNA polymerase purified from *Thermus aquaticus* and recombinant means for producing the enzyme. Thermostable DNA polymerases are useful in many recombinant DNA techniques, especially nucleic acid amplification by the polymerase chain reaction (PCR).

Directed protein-evolution strategies generally make use of a link between a protein and the encoding DNA. In phage-display technology, this link is provided by fusion of the protein with a coat-protein that is incorporated into the phage particle containing the DNA. Optimization of this link can be achieved by adjusting the signal sequence of the fusion.

Linking of a gene to its corresponding polypeptide is a central step in directed protein evolution toward new functions. Filamentous bacteriophage particles have been extensively used to establish this linkage between a gene of interest and its protein expressed as a fusion product with a phage coat protein for incorporation into the phage particle. Libraries of proteins displayed on phage can be subjected to in vitro selection to isolate proteins with desired properties together with their genes.

Creating a link between a gene and a single corresponding protein was achieved by making use of a phagemid for expression of the fusion protein and of a helper phage for assembly of the phage particles. This approach, yielding a monovalent display of protein, was found to be essential to avoid avidity effects or chelate effects, which introduce strong biases during in vitro selections for affinity. However, it also produces phage particles that do not display any protein of interest and which thereby represent a background in evolution experiments.

To optimize the link between a gene and a single corresponding protein, several methods have been used. For example, the periplasmic factor Skp was found to improve the display of single-chain Fv antibodies on filamentous phage (Bothmann, H. and Plückthun, A., 1998). In a previous study, the present inventors showed that specific signal sequences for optimal display on phage of the Taq DNA polymerase I Stoffel

fragment can be isolated from a library of more than 10^7 signal sequences derived from pelB (Jestin, J.L., Volioti, G. and Winter, G., 2001). Signal sequences, once translated, are recognized by the bacterial protein export machinery. The polypeptide is then exported in the bacterial periplasm before cleavage of the signal peptide by the signal peptidase, thereby releasing the mature protein.

A short sequence, *m* (SG_4CG_4; residues 3-12 of SEQ ID NO: 39), at the C-terminus of the signal sequence, was initially introduced as a potential cross-linking site of substrates on phage that may be useful for selections by catalytic activity. This glycine-rich sequence may also be important for preventing structure formation at the peptidase cleavage site or for defining two independently folding units in the pre-protein. The glycine-rich sequence may then improve the signal sequence processing and finally lead to a greater ratio of protein fusions on phage. The present inventors, therefore, evaluated the effect of a selected signal sequence on the display of proteins on phage, as well as the effect of the *m* sequence at the C-terminus of the signal peptide.

In an embodiment of the present invention is a method of identifying thermostable mutant polymerases derived from the Stoffel fragment of Taq comprising:

a) packaging a vector in which a polynucleotide encoding a phage coat protein is fused to a polynucleotide encoding a protein having at least 80% identity to residues 13-555 of SEQ ID NO: 26 into a phage;

b) expressing the fusion protein;

c) isolation (selection) of phage particles;

d) infecting *E. coli* and incubating the infected *E. coli*;

e) detecting the fusion protein;

f) assessing polymerase activity.

In this method, evolutionarily advantageous mutants may be identified by repeating steps (b) – (f) 0 to 25 times, preferably 0-20 times, more preferably 1-15 times, a most preferably 2 to 10 times. The method comprising one cycle (repeated 0 times) is particularly adapted to high throughput screening, when steps are repeated from 3 to 7 times, the method is better adapted for classical empirical screening.

In a preferred embodiment, the phage coat protein is fused to said polynucleotide encoding a protein having at least 80% identity to residues 13-555 of

SEQ ID NO: 26 by way of a linker having a sequence represented by residues 3-12 of SEQ ID NO: 39.

By way of example, Applicants provide the following exemplary discussion of the phage-display method of the present invention and refer to Strobel et al., 2003, which is incorporated herein by reference in its entirety:

The amino acid signal sequences are that may be attached to the N-terminus of the proteins of the present invention:

pelB: MKYLLPTAAAGLLLLAAQPAMA (SEQ ID NO: 41);
l7: MKTLLAMVLVGLLLLPPGPSMA (SEQ ID NO: 42);
l10: MRGLLAMLVAGLLLLPIAPAMA (SEQ ID NO: 43); and
l12: MRRLLVIAAVGLLLLLAPPTMA (SEQ ID NO: 44).

The present inventors goal was to increase the display of proteins at the surface of filamentous phages. As model proteins, the present inventors chose the catalytic domains of adenylate cyclases from *E. coli* (ACE) and from *B. pertussis (*ACB). The present inventors also examined the display of two different enzymes, an adenylate cyclase and the Stoffel fragment of Taq DNA polymerase I, incorporated into phage particles as single polypeptide fusion products with minor coat protein p3. In this work, the present inventors evaluated the effects of two signal peptides (pelB and l7) and of the short peptide (*m*; residues 3-12 of SEQ ID NO: 39) at the N-terminus of the fusion of these enzymes with p3. One other construct, deriving from the selected signal peptide l12, is also mentioned here, and the data are summarized together with previously published data for the selected signal sequences l10 and l12 (Jestin et al., 2001).

The phage particles were produced by using a helper phage, KM13 (Kristensen et al., 1998), for assembly of the particles, and by using phagemids pHEN1 (Hoogenboom, H.R., Griffiths, A.D., Johnson, K.S., et al., 1991), pHEN1l7, and pHEN1l12 (Jestin et al., 2001) encoding the p3 fusion proteins. These phagemid vectors differ in their signal sequence: pelB is from Erwinia caratovora pectate lyase B (Lei, S.P., Lin, H.C., Wang, S.S., Callaway, J., et al., 1987), whereas signal sequences l7, l10, and l12, were selected from a library of more than 10^7 signal sequences for optimal display of the Stoffel fragment on filamentous phage (Jestin et al., 2001). For all 17 phagemids encoding the different fusion proteins described in this work, the present inventors observed standard titers of infective particles, which were all in the

range of 1.4×10^{10}-7.8×10^{10} phages/mL of culture medium. Furthermore, enzymatic activities were detected for all phage-cyclase particles by thin layer chromatography and by HPLC (data not shown).

The efficiency of protein display on phage was evaluated through two approaches. The first makes use of the engineered helper phage KM13 (Kristensen et al., 1998) to measure the fraction of infective phage particles that display a fusion product. The p3 fusion protein provided by the phagemid and the p3 protein provided by the helper phage compete for incorporation into the phage particles. The helper phage p3 is engineered so as to contain a protease cleavage site between domains 2 and 3 of p3. In phage particles that contain only helper p3 copies, no full p3 copy is available for bacterial infection after protease treatment: the phage particles are noninfective. If a phage particle has incorporated a p3 fusion protein, one copy of the three-p3 domains remains after protease cleavage, and is sufficient for infection of *E. coli*. The trypsin-resistant fraction of phage is therefore a measure of protein display on infective phages. With this method, the display of fusion proteins was found to vary over more than two orders of magnitude for each cyclase, depending on the signal sequence and on neighboring sequences. Among the phagemid vectors containing the selected signal sequence 17, three of the four fusion proteins that the present inventors studied (AC-p3 and AC-Stoffel-p3, where AC is the adenylate cyclase catalytic domain of *E. coli* or *B. pertussis*) were remarkably well incorporated into phage particles: more than one phage particle out of ten displayed an enzyme. No more than one particle in 300 displayed the *E. coli* cyclase fused to the Stoffel fragment and to protein 3, and better display of this protein could not be found among the constructs tested.

The peptide *m*, SG_4CG_4, at the N-terminus of the mature fusion protein, was found to increase the display of *B. pertussis* cyclase-polymerase fusion on phage, by 100-fold for signal sequence 17 and by 10-fold for *pel*B. For this fusion, the worst display ratios are significantly improved with peptide *m*. Display of *B. pertussis* cyclase on phage was high in all cases, such that a marginal improvement due to the *m* peptide was found for signal sequence 17, and improvement within the limits of experimental error for *pel*B. Concerning the *E. coli* cyclase protein, peptide *m* decreases the latter's display by a factor of 30 to 40. For the *E. coli* cyclase-polymerase fusion, peptide *m*

showed no significant effect with the signal sequence pelB and a small improvement with signal sequence 17.

Significant effects of the signal sequence on phage display were detected for three of the four fusions in the present inventors' study: from 5- to about 20-fold improvements in display on phage were noted for substitution of pelB by signal sequence 17. In the case of the *B. pertussis* cyclase-p3 fusion protein, incorporation of the fusion protein into phage particles was high, whether the signal sequence was pelB, 17, or 112. Indeed, for the selected signal sequence 112, up to 40% of infective phage particles displayed an enzyme at the surface of filamentous phage.

When two enzymes were simultaneously displayed on phage (either *E. coli* or *B. pertussis* adenylate cyclase and the Stoffel fragment polymerase), the present inventors noted that the incorporation of p3 fusion products was significantly reduced in most cases. Remarkably, about half of the infective phage particles displayed a *B. pertussis* adenylate cyclase-Stoffel fragment polymerase–p3 protein fusion when the selected signal sequence 17 and the short N-terminal peptide *m* were present in the construct.

The second approach to estimating the level of fusion proteins incorporated into phage particles relies on the detection of p3 domain 3 by a monoclonal antibody (Tesar, M., Beckmann, C., Rottgen, P., et al., 1995) after SDS-PAGE and Western blotting of denatured phage particles. These results are in accordance with the data the present inventors obtained by measuring the trypsin-resistant fraction of infective phages. All fusion products expressed on phage and which correspond to a trypsin-resistant fraction of phage higher than 0.1 are indeed observed by Western blot analysis.

The present inventors aim to direct the evolution of adenylate cyclases by in vitro selection using a chemistry involving filamentous phage. This should provide a tool for the engineering of adenylate cyclases as well as a strategy for the functional cloning of this class of enzymes. Recent in vitro selection methods for catalytic activity using phage display have been designed as affinity chromatography methods for the reaction product linked to the phageenzyme that catalyzed the reaction from substrate to product. These selection methods were established with enzymes such as nuclease (Pedersen, H., Hölder, S., Sutherlin, D.P., et al., 1998), DNA polymerase (Jestin et al., 1999), peptidase (Dematris, S., Huber, A., et al., 1999; Heinis, C., Huber, A. et al., 2001), peptide ligase (Atwell et al., 1999), and beta-lactamase (Ponsard et al., 2001).

They require an efficient display of enzyme on phage and a method to link the substrate/product to phage-enzymes.

In the work reported here, the present inventors investigated the display of adenylate cyclases from *B. pertussis* and from *E. coli* on filamentous phage, and the display of two independent enzymes, an adenylate cyclase and the Taq DNA polymerase I Stoffel fragment. The Stoffel fragment (Lawyer, F.C., Stoffel, S., Saiki, R.K., et al., 1989) could be used as a tool to establish an in vitro selection for cyclase activity as follows: the polymerase domain may serve as an anchor of the substrate ATP on phage through double-stranded DNA used as a linker with a high affinity for the fusion protein. Another approach to cross-linking substrate and phage involves introduction of the thiol group of a cysteine residue within peptide *m* (SG_4CG_4), at the N-terminus of the mature fusion protein and at the C-terminus of the fusion protein's signal sequence (Jestin et al., 1999).

The signal sequences 17, 110, and 112, used in the present inventors' study had been selected from large libraries of pelB mutants for optimal display of the Stoffel fragment-p3 protein fused to the peptide *m* (Jestin et al., 2001). It was therefore important to further investigate which sequence context was essential for selection of these signal sequences, either the short peptide *m* or the entire gene. Interestingly, the present inventors found that the presence or the absence of this short peptide, SG_4CG_4, can yield up to 100-fold increases in the display of a fusion protein on filamentous phage. This strong effect was observed for the *B. pertussis* cyclase-Stoffel-p3 fusion as well as for the *E. coli* cyclase-p3 fusion in the case of the signal sequence 17 (Table 2). Of further note is that the signal sequences 17 and 112, yield generally better levels of protein display on phage than does pelB (Figure 3). This improved display of proteins might be ascribed to the different targeting modes of the signal sequences. These selected signal sequences that improve the display of proteins on phage should therefore be useful in other systems.

Our study highlights the important effects of the signal sequence and of a short peptide at the C-terminus of the signal sequence on the display of proteins on phage. Apart from the previously stated conclusions that the selected signal sequence 17 often yields an improved display as compared with pelB, and that sequence *m* can have drastic effects on the level of protein display, the set of protein fusions described here is

not sufficient to define any further rules about sequences and optimal display of proteins on phage. Indeed, incorporation of a fusion protein into a phage particle is the result of a complex sequence of events involving fusion gene transcription and translation, folding, and export of the fusion protein, as well as cleavage of the signal sequence.

Two approaches, however, can be envisaged for efficient display of proteins on bacteriophage. First, directed signal peptide evolution experiments can be undertaken for any defined protein so as to isolate a signal sequence for optimal display on phage. This approach was described previously in the case of the Stoffel fragment of Taq DNA polymerase I (Jestin et al., 2001). A more straightforward and quicker approach consists of the screening of several phagemid vectors that differ in their signal sequences and, more generally, in their regulatory sequences. In this report the present inventors have shown that for three of the four fusion proteins tested, excellent cyclase display levels can be obtained: more than one phage in ten displays an enzyme. Such display levels for large proteins should be useful for further approaches to directed protein evolution.

With use of the phagemid strategy, almost every particle expresses a p3 copy provided by the phagemid if no gene fusion has been engineered or if the insert from the gene fusion has been deleted. On the contrary, about one phage particle in a thousand incorporates large fusion proteins such as cyclase-Stoffel fragment-p3 fusions. This indicates that for an equal mixture of two genes, thousand-fold differences in expression of the corresponding proteins on phage particles can be obtained. This bias may be of no importance if enrichment factors per selection round are much larger than 10^3, but it may otherwise significantly alter the outcome of evolution experiments. Similar protein expression levels on phage of different genes would be useful to minimize biases introduced by successive amplifications in evolution experiments. The use of sets of phagemid vectors that differ by their signal sequences and by neighboring sequences might be of interest for better representation of protein libraries on filamentous phage. Additionally, the display of two distinct enzymes on single phage particles might be useful to direct their coevolution, especially in the case of two enzymes involved in the same metabolic pathway with an unstable reaction intermediate.

By insertion or by deletion of the short peptide sequence SG_4CG_4 (*m*; residues 3-12 of SEQ ID NO: 39) at the C-terminus of the signal sequence (i.e., immediately upstream (N-terminal) to the variant Stoffel fragments of the present invention), the

present inventors have shown that two enzymes can be very efficiently expressed as single polypeptides on the surface of filamentous bacteriophage by using the phagemid strategy. The model proteins described in this study are the catalytic domains of adenylate cyclases of *B. pertussis* or of *E. coli*, fused or not fused to the Stoffel-fragment DNA polymerase.

On average, the present inventors found the best display levels for the selected signal sequence 17, which had been previously selected from a large library for optimal display on phage of the Stoffel fragment, and not for the commonly used signal sequence pelB. Yet the present inventors observed striking differences in display levels of these enzymes on the surfaces of phage particles, depending on the short N-terminal peptide m. The findings reported here should be useful for the display of large and of cytoplasmic proteins on filamentous phage particles, and more generally for protein engineering using phage display.

It is important to note that within the present application the terms "protein," "polymerase," "enzyme," "clone," and "variant" are considered to be equivalent terms when used to qualify, name, or otherwise designate the mutant Stoffel fragments of the present invention. Further, in the context of the present invention the term "Stoffel fragment," "the Stoffel fragment of DNA polymerase I obtained from *Thermus aquaticus*" or similar terms are used herein, and is frequently associated with SEQ ID NO: 26. Also in the present invention variant **e** is used in conjunction with SEQ ID NO: 26, as this sequence corresponds to the native Stoffel fragment of DNA polymerase I obtained from *Thermus aquaticus*, but contains a R518G (in the context of the full-length Taq sequence, this is a R795G mutation). It is to be understood that reference to variant **e** is sometimes used as a short hand for residues 13-555 of SEQ ID NO: 26, wherein SEQ ID NO: 26 actually corresponds to the native Stoffel fragment of DNA polymerase I obtained from *Thermus aquaticus*.

Residues 1-12 of SEQ ID NO: 26 correspond to SEQ ID NO: 39, which contain 2 residues from the signal sequence (MetAla) and 10 residues ($SerGly_4CysGly_4$) corresponding to a linker that had been introduced at N-terminus of the mature fusion protein on phage so as to introduce a cysteine residue that might be important for substrate cross-linking on phage. Further residues 556-562 correspond to residues 1-7 of SEQ ID NO: 40, which is the resultant sequence following thrombin cleavage of the

sequence of SEQ ID NO: 40. It should also be understood that the present invention embraces sequences corresponding to residues 13-555 of SEQ ID NO: 26 as defined herein, as well as sequences in which the N-terminus and C-terminus contain signal sequences, linker sequences, purification tags, and/or fusion constructs.

The term "thermostable" enzyme refers to an enzyme that is stable over a temperature range of approximately 55°C to 105°C. In particular, thermostable enzymes in accordance with the present invention are heat resistant and catalyze the template directed DNA synthesis. Preferably, the activity of the thermostable enzymes of the present is at least 50% of activity, preferably at least 75%, more preferably at least 85%, of the wild-type enzyme activity over the same temperature range. In a particularly preferred embodiment, the thermostable enzyme of the present invention exhibits at least 50% of activity, preferably at least 75%, more preferably at least 85%, of the wild-type enzyme activity when said wild-type enzyme activity is measured under optimal conditions. Moreover, it is preferable that the "thermostable" enzyme does not become irreversibly denatured when subjected to the elevated temperatures and incubation time for denaturation of double-stranded nucleic acids, as well as the repetitive cycling between denaturation, annealing, and extension inherent to PCR-based techniques.

As used herein, the term "reduced" or "inhibited" means decreasing the activity of one or more enzymes either directly or indirectly. The definition of these terms also includes the reduction of the *in vitro* activity, either directly or indirectly, of one or more enzymes.

The term "enhanced" as used herein means increasing the activity or concentration one or more polypeptides, which are encoded by the corresponding DNA. Enhancement can be achieved with the aid of various manipulations of the bacterial cell, including mutation of the protein, replacement of the expression regulatory sequence, etc.

In order to achieve enhancement, particularly over-expression, the number of copies of the corresponding gene can be increased, a strong promoter can be "operably linked," or the promoter- and regulation region or the ribosome binding site which is situated upstream of the structural gene can be mutated. In this regard, the term "operably linked" refers to the positioning of the coding sequence such that a promoter,

regulator, and/or control sequence will function to direct the expression of the protein encoded by the coding sequence located downstream therefrom.

Expression cassettes that are incorporated upstream of the structural gene act in the same manner. In addition, it is possible to increase expression by employing inducible promoters. A gene can also be used which encodes a corresponding enzyme with a high activity. Expression can also be improved by measures for extending the life of the mRNA. Furthermore, preventing the degradation of the enzyme increases activity as a whole. Moreover, these measures can optionally be combined in any desired manner. The definition of these terms also includes the enhancement of the *in vitro* activity, either directly or indirectly, of one or more enzymes.

It is to be understood that the in addition to the following variant Stoffel polypeptides and polynucleotides encoding the same, the present invention also embraces full-length Taq polymerase enzymes in which the specifically identified mutations have been effectuated. The present invention further embraces full-length polymerases beyond those of the genus *Thermus* in which the domain equivalent in function to the Stoffel fragment is replaced by the variant sequences of the present invention thereby imparted or enhancing thermostability of the resultant polymerase. The skilled artisan would readily appreciate methods of mutagenesis and/or sub-cloning to alter the sequence of the Taq polymerase to incorporate the same. Further, the references cited herein, such as Maniatis, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, p. 412 (1982), provide such techniques.

A gene (polynucleotide) can be used which encodes a corresponding or variant polymerase having at least 80% homology to amino acid residues 13-555 of SEQ ID NO: 26. These genes (polynucleotides) can encode various mutations. For example, a mutation of one or more amino acids in amino acids 461-490 of SEQ ID NO:26 (738 to 767 of the Taq polymerase wild-type sequence SEQ ID NO: 100). Further examples of mutations include mutations at positions M470, F472, M484, and W550, A331, and S335. In a preferred embodiment, the mutation may be at least one of H203, F205, T232, E253, Q257, D274, L275, I276, V309, I322, A331, L332, D333, Y334, S335, I361, R374, A384, T387, Y419, P493, M498, G499, M502, L503, V506, R518, A523, A526, P539, E543, and W550.

In a preferred embodiment, these mutations are A331T, S335N, M470K, M470R, F472Y, M484V, M484T, and W550R. In a particularly preferred embodiment, the polynucleotides of the present invention encode polypeptides having one or more of the aforementioned mutations and share at least 85% identity, at least 90% identity, at least 95% identity, or at least 97.5% identity to the polypeptide comprising amino acid residues 13-555 of SEQ ID NO: 26. Moreover, polynucleotides of the present invention encode polypeptides that have DNA polymerase activity and/or 5'-3' exonuclease activity. More particularly, the polynucleotides of the present invention encode polypeptides that are capable of catalyzing the reverse transcription of RNA.

In the present invention, the polynucleotide may encode a polypeptide contain at least one mutation at a position selected from the group consisting of A331, L332, D333, Y334, and S335.

The polynucleotide may encode a polypeptide of the present invention which has amino acid sequence of residues 13-555 of a sequence selected from the group consisting of SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, and SEQ ID NO: 38.

Within the context of the present application, the preferred polynucleotides possess a polynucleotide sequence corresponding to nucleotides 39-1667 of a sequence selected from the group consisting of SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, and SEQ ID NO: 37.

In another embodiment of the present invention, are thermostable polypeptides having at least 80% homology, preferably at least 90%, more preferably at least 95%, most preferably at least 97.5%, to residues 13-555 of SEQ ID NO: 26, wherein said polypeptide has at least one mutation selected from the group consisting of H203R (position 480 of the Taq polymerase wild-type sequence SEQ ID NO: 100), F205L (position 482 of the Taq polymerase wild-type sequence SEQ ID NO: 100), T232S (position 509 of the Taq polymerase wild-type sequence SEQ ID NO: 100), E253G (position 530 of the Taq polymerase wild-type sequence SEQ ID NO: 100), Q257R (position 534 of the Taq polymerase wild-type sequence SEQ ID NO: 100), D274G (position 551 of the Taq polymerase wild-type sequence SEQ ID NO: 100), L275H (position 552 of the Taq polymerase wild-type sequence SEQ ID NO: 100), L275P

(position 552 of the Taq polymerase wild-type sequence SEQ ID NO: 100), I276F (position 553 of the Taq polymerase wild-type sequence SEQ ID NO: 100), V309I (position 586 of the Taq polymerase wild-type sequence SEQ ID NO: 100), I322N (position 599 of the Taq polymerase wild-type sequence SEQ ID NO: 100), A331V (position 608 of the Taq polymerase wild-type sequence SEQ ID NO: 100), S335N (position 612 of the Taq polymerase wild-type sequence SEQ ID NO: 100), I361F (position 638 of the Taq polymerase wild-type sequence SEQ ID NO: 100), R374Q (position 651 of the Taq polymerase wild-type sequence SEQ ID NO: 100), A384T (position 661 of the Taq polymerase wild-type sequence SEQ ID NO: 100), T387A (position 664 of the Taq polymerase wild-type sequence SEQ ID NO: 100), Y419C (position 696 of the Taq polymerase wild-type sequence SEQ ID NO: 100), Y419N (position 696 of the Taq polymerase wild-type sequence SEQ ID NO: 100), E465K (position 742 of the Taq polymerase wild-type sequence SEQ ID NO: 100), M470K (position 747 of the Taq polymerase wild-type sequence SEQ ID NO: 100), M470R (position 747 of the Taq polymerase wild-type sequence SEQ ID NO: 100), F472Y (position 749 of the Taq polymerase wild-type sequence SEQ ID NO: 100), F472S (position 749 of the Taq polymerase wild-type sequence SEQ ID NO: 100), A487T (position 764 of the Taq polymerase wild-type sequence SEQ ID NO: 100), K490E (position 767 of the Taq polymerase wild-type sequence SEQ ID NO: 100), P493T (position 770 of the Taq polymerase wild-type sequence SEQ ID NO: 100), M498T (position 775 of the Taq polymerase wild-type sequence SEQ ID NO: 100), G499E (position 776 of the Taq polymerase wild-type sequence SEQ ID NO: 100), M502K (position 779 of the Taq polymerase wild-type sequence SEQ ID NO: 100), L503P (position 780 of the Taq polymerase wild-type sequence SEQ ID NO: 100), V506I (position 783 of the Taq polymerase wild-type sequence SEQ ID NO: 100), A523V (position 800 of the Taq polymerase wild-type sequence SEQ ID NO: 100), A526V (position 803 of the Taq polymerase wild-type sequence SEQ ID NO: 100), P539S (position 816 of the Taq polymerase wild-type sequence SEQ ID NO: 100), E543K (position 820 of the Taq polymerase wild-type sequence SEQ ID NO: 100), and W550R (position 827 of the Taq polymerase wild-type sequence SEQ ID NO: 100), and wherein said polypeptide has improved DNA polymerase activity and retains 5'-3' exonuclease

activity. In an object of the present invention, the 3'-5' exonuclease activity of the mutant polypeptide is inactive.

Moreover, the present invention provides for polynucleotides that encode for the aforementioned thermostable polypeptides within this embodiment.

In the present invention, the polynucleotide may encode a polypeptide having a sequence of residues 1-543 from a sequence selected from the group consisting of SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, and SEQ ID NO: 99.

Within the context of the present application, the preferred polynucleotides possess a polynucleotide sequence corresponding to nucleotides 1-1629 of a sequence selected from the group consisting of SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, and SEQ ID NO: 98.

In another embodiment of the present invention, the mutant DNA polymerase has a sequence corresponding to residues 1-543 of one of the following sequences: SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, and SEQ ID NO: 99.

Within the scope of the present invention are also polynucleotides that are homologous to the aforementioned sequences. In the context of the present application, a polynucleotide sequence is "homologous" with the sequence according to the invention if at least 80%, preferably at least 90%, more preferably 95%, and most preferably 97.5% of its base composition and base sequence corresponds to the sequence according to the invention. It is to be understood that, as evinced by the Examples of the present invention and the phage-display method highlighted herein, screening of theoretical mutations within the scope of the present invention would require nothing more than a technician's level of skill in the art. More specifically, as is

routine in the art, with the identification of a candidate sequence the artisan would assay and screen one or all possible permutations of the said sequence to identify mutants possessing the same or better DNA polymerase activity, reverse transcriptase activity, and/or 5'-3' exonuclease activity.

The expression "homologous amino acids" denotes those that have corresponding properties, particularly with regard to their charge, hydrophobic character, steric properties, etc.

Homology, sequence similarity or sequence identity of nucleotide or amino acid sequences may be determined conventionally by using known software or computer programs such as the *BestFit* or *Gap* pairwise comparison programs (GCG Wisconsin Package, Genetics Computer Group, 575 Science Drive, Madison, Wisconsin 53711). *BestFit* uses the local homology algorithm of Smith and Waterman, Advances in Applied Mathematics 2: 482-489 (1981), to find the best segment of identity or similarity between two sequences. *Gap* performs global alignments: all of one sequence with all of another similar sequence using the method of Needleman and Wunsch, J. Mol. Biol. 48:443-453 (1970). When using a sequence alignment program such as *BestFit*, to determine the degree of sequence homology, similarity or identity, the default setting may be used, or an appropriate scoring matrix may be selected to optimize identity, similarity or homology scores. Similarly, when using a program such as *BestFit* to determine sequence identity, similarity or homology between two different amino acid sequences, the default settings may be used, or an appropriate scoring matrix, such as *blosum45* or *blosum80*, may be selected to optimize identity, similarity or homology scores.

The terms "isolated" or "purified" means separated from its natural environment.

The term "polynucleotide" refers in general to polyribonucleotides and polydeoxyribonucleotides, and can denote an unmodified RNA or DNA or a modified RNA or DNA.

The term "polypeptides" is to be understood to mean peptides or proteins that contain two or more amino acids that are bound via peptide bonds. A "polypeptide" as used herein is understood to mean a sequence of several amino acid residues linked by peptide bonds. Such amino acids are known in the art and encompass the unmodified

and modified amino acids. In addition, one or more modifications known in the art such as glycosylation, phosphorylation, etc may modify the polypeptide.

The term "homologous" as used herein is understood to mean two or more proteins from the same species or from a different species. Within the meaning of this term, said two or more polypeptides share at least 80% identity to residues 13-555 of the polypeptide of SEQ ID NO: 26 and can have the mutations discussed herein. In a particularly preferred embodiment, the polypeptides of the present invention have one or more of the aforementioned mutations and share at least 85% identity, at least 90% identity, at least 95% identity, or at least 97.5% identity to residues 13-555 of the polypeptide of SEQ ID NO: 26. Moreover, the polypeptides of the present invention have DNA polymerase activity and/or 5'-3' exonuclease activity. More particularly, the polypeptides of the present invention are capable of catalyzing the reverse transcription of mRNA.

In the present invention, the polypeptide may contain one or more mutations, such as A331, L332, D333, Y334, and S335.

The isolated polypeptide of the present invention has an amino acid sequence corresponding to residues 13-555 of a sequence selected from the group consisting of SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, and SEQ ID NO: 38.

Further, the mutant DNA polymerase may have a sequence corresponding to residues 1-543 of one of the following sequences: SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, and SEQ ID NO: 99.

In an embodiment of the present invention are mutations concerning alanine in position 331 (A331), and serine in position 335 (S335) that may have particular importance derived from the fact that they are surrounding the aspartic acid D in position 333 which is responsible for the chelation of Mn^{2+} or Mg^{2+}. Thus, in one embodiment of the present invention, mutations of one or more amino acids 10 amino acids upstream and/or 10 amino acids downstream of this site are provided.

The expression "homologous amino acids" denotes those that have corresponding properties, particularly with regard to their charge, hydrophobic character, steric properties, etc.

Moreover, one skilled in the art is also aware of conservative amino acid replacements such as the replacement of glycine by alanine or of aspartic acid by glutamic acid in proteins as "sense mutations" which do not result in any fundamental change in the activity of the protein, i.e. which are functionally neutral. It is also known that changes at the N- and/or C-terminus of a protein do not substantially impair the function thereof, and may even stabilize said function. As such, these conservative amino acid replacements are also envisaged as being within the scope of the present invention.

The present invention also relates to DNA sequences that hybridize with the DNA sequence that encodes a corresponding or variant polymerase having at least 80% homology, preferably at least 90%, more preferably at least 95%, most preferably at least 97.5%, to residues 13-555 of SEQ ID NO: 26, the polypeptides having the mutations described herein. The present invention also relates to DNA sequences that are produced by polymerase chain reaction (PCR) using oligonucleotide primers that result from the DNA sequence that encodes a corresponding or variant polymerase having at least 80% homology, preferably at least 90%, more preferably at least 95%, most preferably at least 97.5%, to residues 13-555 of SEQ ID NO: 26, wherein the polypeptide has at least one mutation as described herein, or fragments thereof. Oligonucleotides of this type typically have a length of at least 15 nucleotides.

The terms "stringent conditions" or "stringent hybridization conditions" includes reference to conditions under which a polynucleotide will hybridize to its target sequence, to a detectably greater degree than other sequences (e.g., at least 2-fold over background). As used herein, stringent hybridization conditions are those conditions which allow hybridization between polynucleotides that are 80%, 85%, 90%, 95%, or 97.5% homologous as determined using conventional homology programs, an example of which is UWGCG sequence analysis program available from the University of Wisconsin. (Devereaux et al., 1984). Stringent conditions are sequence-dependent and will be different in different circumstances. By controlling the stringency of the hybridization and/or washing conditions, target sequences can be identified which are

100% complementary to the probe (homologous probing). Alternatively, stringency conditions can be adjusted to allow some mismatching in sequences so that lower degrees of similarity are detected (heterologous probing).

Typically, stringent conditions will be those in which the salt concentration is less than about 1.5 M Na ion, typically about 0.01 to 1.0 M Na ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (e.g., 10 to 50 nucleotides) and at least about 60 °C for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. Exemplary low stringency conditions include hybridization with a buffer solution of 30 to 35% formamide, 1 M NaCl, 1% SDS (sodium dodecyl sulfate) at 37 °C, and a wash in 1X to 2X SSC (20X SSC=3.0 M NaCl/0.3 M trisodium citrate) at 50 to 55°C Exemplary moderate stringency conditions include hybridization in 40 to 45% formamide, 1 M NaCl, 1% SDS at 37 °C, and a wash in 0.5X to 1X SSC at 55 to 60°C. Exemplary high stringency conditions include hybridization in 50% formamide, 1 M NaCl, 1% SDS at 37 °C, and a wash in 0.1X SSC at 60 to 65°C.

Specificity is typically the function of post-hybridization washes, the critical factors being the ionic strength and temperature of the final wash solution. For DNA--DNA hybrids, the Tm can be approximated from the equation of Meinkoth and Wahl, Anal. Biochem., 138:267-284 (1984): Tm =81.5°C +16.6 (log M)+0.41 (%GC)-0.61 (% form)-500/L; where M is the molarity of monovalent cations, %GC is the percentage of guanosine and cytosine nucleotides in the DNA, % form is the percentage of formamide in the hybridization solution, and L is the length of the hybrid in base pairs. The Tm is the temperature (under defined ionic strength and pH) at which 50% of a complementary target sequence hybridizes to a perfectly matched probe. Tm is reduced by about 1°C for each 1% of mismatching; thus, Tm, hybridization and/or wash conditions can be adjusted to hybridize to sequences of the desired identity. For example, if sequences with approximately 90% identity are sought, the Tm can be decreased 10°C. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (Tm) for the specific sequence and its complement at a defined ionic strength and pH. However, severely stringent conditions can utilize a hybridization and/or wash at 1, 2, 3, or 4°C lower than the thermal melting point (Tm);

moderately stringent conditions can utilize a hybridization and/or wash at 6, 7, 8, 9, or 10°C lower than the thermal melting point (Tm); low stringency conditions can utilize a hybridization and/or wash at 11, 12, 13, 14, 15, or 20°C lower than the thermal melting point (Tm). Using the equation, hybridization and wash compositions, and desired Tm, those of ordinary skill will understand that variations in the stringency of hybridization and/or wash solutions are inherently described. If the desired degree of mismatching results in a Tm of less than 45°C (aqueous solution) or 32°C (formamide solution) it is preferred to increase the SSC concentration so that a higher temperature can be used. An extensive guide to the hybridization of nucleic acids is found in Current Protocols in Molecular Biology, Chapter 2, Ausubel, et al., Eds., Greene Publishing and Wiley-Interscience, New York (2000).

Thus, with the foregoing information, the skilled artisan can identify and isolated polynucleotides, which are substantially similar to the present polynucleotides. In isolating such a polynucleotide, the polynucleotide can be used as the present polynucleotide in, for example, to express a polypeptide having DNA polymerase activity and 5'-3' exonuclease activity.

One embodiment of the present invention is methods of screening for polynucleotides, which have substantial homology to the polynucleotides of the present invention, preferably those polynucleotides encoding a polypeptide having DNA polymerase activity and/or 5'-3' exonuclease activity.

The polynucleotide sequences of the present invention can be carried on one or more suitable plasmid vectors, as known in the art for bacteria or the like.

Host cells useful in the present invention include any cell having the capacity to be infected or transfected by phages or vectors comprising the polynucleotide sequences encoding the enzymes described herein and, preferably also express the thermostable enzymes as described herein. Suitable host cells for expression include prokaryotes, yeast, archae, and other eukaryotic cells. Appropriate cloning and expression vectors for use with bacterial, fungal, yeast, and mammalian cellular hosts are well known in the art, *e.g.*, Pouwels *et al.* (1985). The vector may be a plasmid vector, a single or double-stranded phage vector, or a single or double-stranded RNA or DNA viral vector. Such vectors may be introduced into cells as polynucleotides, preferably DNA, by well known techniques for introducing DNA and RNA into cells. The vectors, in the case of

phage and viral vectors also may be and preferably are introduced into cells as packaged or encapsulated virus by well-known techniques for infection and transduction. Viral vectors may be replication competent or replication defective. In the latter case viral propagation generally will occur only in complementing host cells. Cell-free translation systems could also be employed to produce the enzymes using RNAs derived from the present DNA constructs.

Prokaryotes useful as host cells in the present invention include gram negative or gram-positive organisms such as E. *coli* or *Bacilli*. In a prokaryotic host cell, a polypeptide may include a N-terminal methionine residue to facilitate expression of the recombinant polypeptide in the prokaryotic host cell. The N-terminal Met may be cleaved from the expressed recombinant polypeptide. Promoter sequences commonly used for recombinant prokaryotic host cell expression vectors include β-lactamase and the lactose promoter system.

Expression vectors for use in prokaryotic host cells generally comprise one or more phenotypic selectable marker genes. A phenotypic selectable marker gene is, for example, a gene encoding a protein that confers antibiotic resistance or that supplies an autotrophic requirement. Examples of useful expression vectors for prokaryotic host cells include those derived from commercially available plasmids such as the cloning vector pBR322 (ATCC 37017). pBR322 contains genes for ampicillin and tetracycline resistance and thus provides simple means for identifying transformed cells. To construct an expression vector using pBR322, an appropriate promoter and a DNA sequence are inserted into the pBR322 vector.

Other commercially available vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and pGEM1 (Promega Biotec, Madison, Wisconsin., USA).

Promoter sequences commonly used for recombinant prokaryotic host cell expression vectors include β-lactamase (penicillinase), lactose promoter system (Chang et al., 1978; and Goeddel et al., 1979), tryptophan (trp) promoter system (Goeddel et al., 1980), and tac promoter (Maniatis, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, p. 412 (1982)).

Yeasts useful as host cells in the present invention include those from the genus Saccharomyces, Pichia, K. Actinomycetes and Kluyveromyces. Yeast vectors will often

contain an origin of replication sequence from a 2μ yeast plasmid, an autonomously replicating sequence (ARS), a promoter region, sequences for polyadenylation, sequences for transcription termination, and a selectable marker gene. Suitable promoter sequences for yeast vectors include, among others, promoters for metallothionein, 3-phosphoglycerate kinase (Hitzeman et al., 1980) or other glycolytic enzymes (Holland et al., 1978) such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvatee decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase. Other suitable vectors and promoters for use in yeast expression are further described in Fleer et al., Gene, 107:285-195 (1991). Other suitable promoters and vectors for yeast and yeast transformation protocols are well known in the art.

Those of skill in the art are familiar with yeast transformation protocols that may be employed in the present invention. One such protocol is described by Hinnen et al., (1978). The Hinnen protocol selects for Trp^+ transformants in a selective medium, wherein the selective medium consists of 0.67% yeast nitrogen base, 0.5% casamino acids, 2% glucose, 10 μg/ml adenine, and 20 μg/ml uracil.

Mammalian or insect host cell culture systems well known in the art could also be employed to express recombinant polypeptides, *e.g.,* Baculovirus systems for production of heterologous proteins in insect cells (Luckow and Summers, (1988)) or Chinese hamster ovary (CHO) cells for mammalian expression may be used. Transcriptional and translational control sequences for mammalian host cell expression vectors may be excised from viral genomes. Commonly used promoter sequences and enhancer sequences are derived from Polyoma virus, Adenovirus 2, Simian Virus 40 (SV40), and human cytomegalovirus. DNA sequences derived from the SV40 viral genome may be used to provide other genetic elements for expression of a structural gene sequence in a mammalian host cell, *e.g.,* SV40 origin, early and late promoter, enhancer, splice, and polyadenylation sites. Viral early and late promoters are particularly useful because both are easily obtained from a viral genome as a fragment which may also contain a viral origin of replication. Exemplary expression vectors for use in mammalian host cells are well known in the art.

The enzymes of the present invention may, when beneficial, be expressed as a fusion protein that has the enzyme attached to a fusion segment. The fusion segment often aids in protein purification, *e.g.*, by permitting the fusion protein to be isolated and purified by affinity chromatography. Fusion proteins can be produced by culturing a recombinant cell transformed with a fusion nucleic acid sequence that encodes a protein including the fusion segment attached to either the carboxyl and/or amino terminal end of the enzyme.

In one embodiment, it may be advantageous for propagating the polynucleotide to carry it in a bacterial or fungal strain with the appropriate vector suitable for the cell type. Common methods of propagating polynucleotides and producing proteins in these cell types are known in the art and are described, for example, in Maniatis et al. (1982) and Sambrook et al. (1989).

In one embodiment of the present invention are monoclonal phages:

1. SJL q deposited under Budapest treaty as CNCM I-3168 in the Collection Nationale de Cultures de Microorganismes (CNCM, Institut Pasteur 25 rue du docteur Roux 75724 Paris cedex 15 France),on February 27, 2004.

2. SJL d deposited under Budapest treaty as CNCM I-3169 in the Collection Nationale de Cultures de Microorganismes (CNCM, Institut Pasteur 25 rue du docteur Roux 75724 Paris cedex 15 France) on February 27, 2004.

3. SJL I deposited under Budapest treaty as CNCM I-3170 in the Collection Nationale de Cultures de Microorganismes (CNCM, Institut Pasteur 25 rue du docteur Roux 75724 Paris cedex 15 France) on February 27, 2004.

4. SJL s deposited under Budapest treaty as CNCM I-3171 in the Collection Nationale de Cultures de Microorganismes (CNCM, Institut Pasteur 25 rue du docteur Roux 75724 Paris cedex 15 France) on February 27, 2004.

5. SJL b deposited under Budapest treaty as CNCM I-3172 in the Collection Nationale de Cultures de Microorganismes (CNCM, Institut Pasteur 25 rue du docteur Roux 75724 Paris cedex 15 France) on February 27, 2004.

6. SJL n deposited under Budapest treaty as CNCM I-3173 in the Collection Nationale de Cultures de Microorganismes (CNCM, Institut Pasteur 25 rue du docteur Roux 75724 Paris cedex 15 France) on February 27, 2004.

7. SJL g deposited under Budapest treaty as CNCM I-3174 in the Collection Nationale de Cultures de Microorganismes (CNCM, Institut Pasteur 25 rue du docteur Roux 75724 Paris cedex 15 France) on February 27, 2004.

8. SJL m deposited under Budapest treaty as CNCM I-3175 in the Collection Nationale de Cultures de Microorganismes (CNCM, Institut Pasteur 25 rue du docteur Roux 75724 Paris cedex 15 France) on February 27, 2004.

9. SJL a deposited under Budapest treaty as CNCM I-3176 in the Collection Nationale de Cultures de Microorganismes (CNCM, Institut Pasteur 25 rue du docteur Roux 75724 Paris cedex 15 France) on February 27, 2004.

10. SVG VIII-176 deposited as CNCM I-3158 in the Collection Nationale de Cultures de Microorganismes (CNCM) on February 10, 2004.

In an embodiment of the present invention is a kit for amplifying DNA containing:

- an isolated thermostable polypeptide, wherein said polypeptide has at least 80% homology to residues 13-555 of SEQ ID NO: 26, wherein said polypeptide has at least one mutation at a position selected from the group consisting of M470, F472, M484, R518, and W550, more preferably selected from the group consisting of M470K, M470R, F472Y, M484V, M484T, R518G, and W550R, and wherein said polypeptide has DNA polymerase activity and 5'-3' exonuclease activity;

- a concentrated buffer solution, wherein when said concentrated buffer is admixed with the isolated polypeptide the overall buffer concentration is 1X;

- one or more divalent metal ions; and

- deoxyribonucleotides.

In this embodiment, the preferred divalent metal ion is Mg^{2+}. In an other embodiment, the metal ion may also be Mn^{2+}. In this connection, the concentration of the divalent metal ion ranges from 0.1 to 5 mM, preferably from 1 to 3 mM, more preferably from 2 to 2.5 mM. However, if the reaction is performed in a phosphate buffer, a buffer containing EDTA, or a buffer containing any other magnesium chelator, the concentration of magnesium may be increased to up to 100 mM.

For the kit of the present invention the isolated thermostable polypeptide may be in a form selected from the group consisting of a lyophilized form, a solution form in a suitable buffer or carrier, and a frozen form in a suitable buffer or carrier.

The kit of the present invention may also include a 5' to 3' exonuclease and/or a 3' to 5' exonuclease. A preferred 5' to 3' exonuclease has a sequence as in SEQ ID NO: 50 (the DNA is in SEQ ID NO: 60) and the 3' to 5' exonuclease as in SEQ ID NO: 51 (the DNA is in SEQ ID NO: 61).

With respect to the suitable buffer or carrier, the following components may be used:

Tris-HCl, KCl, Triton-X100, dimethylsulfoxide, tetramethyl ammonium chloride, etc.

In the present invention, the concentrated buffer solution corresponds to a stock solution that has a concentration ranging from 1.5X to 10X, where the concentration is measured in relation to the final reaction concentration (1X). To this end, the buffer solution (1X) contains the following components: 10 mM Tris-HCl, pH at 25°C of 9, 50 mM KCl, 0.1% Triton-X100.

For the kit according to the present invention, the stock concentration of the deoxyribonucleotides ranges from 50 μM to 200 mM, preferably from 75 μM to 150 mM, more preferably 100 μM to 100 mM, for each dNTP. Moreover, the concentration of each dNTP in the PCR reaction according to the present invention should range from 10 μM to 500 μM, preferably from 25 μM to 400 μM, more preferably 50 μM to 300 μM. As used in the present invention, the term "deoxyribonucleotides" includes: dATP, dCTP, dGTP, and dTTP. It is to be understood that within the scope of the present invention, the kit may include in place of or in addition to the aforementioned components, RNA precursors, minor ("rare") bases, and/or labelled bases.

In another embodiment of the present invention is a method of amplifying DNA from a culture and/or purified stock solution of DNA and/or mRNA by utilizing a thermostable polypeptide according to the present invention. To this end, protocols for conducting PCR and RT-PCR would be readily appreciated by the skilled artisan. However, for sake of completeness, the artisan is directed to the following exemplary references for protocols for conducting PCR and RT-PCR (see, for example, Rougeon, F, et al.; 1975; Rougeon, F, et al., 1976; Grabko, V. I., et al., 1996; and Perler, F., et al., 1996).

With reference to reverse transcribing RNA, a preferred method includes:

a) providing a reverse transcription reaction mixture comprising said RNA, a primer, a divalent cation, and an isolated thermostable polypeptide comprising an amino

acid sequence having at least 80% homology to residues 13-555 of SEQ ID NO: 26, wherein said polypeptide has at least one mutation at a position selected from the group consisting of H203, F205, T232, E253, Q257, D274, L275, I276, V309, I322, A331, L332, D333, Y334, S335, I361, R374, A384, T387, Y419, M470, F472, M484, P493, M498, G499, M502, L503, V506, R518, A523, A526, P539, E543, and W550, more preferably selected from the group consisting of: M470K, M470R, F472Y, M484V, M484T, R518G, and W550R; or H203R, F205L, T232S, E253G, Q257R, D274G, L275H, L275P, I276F, V309I, I322N, A331V, S335N, I361F, R374Q, A384T, T387A, Y419C, Y419N, E465K, M470K, M470R, F472Y, F472S, A487T, K490E, P493T, M498T, G499E, M502K, L503P, V506I, R518G, A523V, A526V, P539S, E543K, and W550R, and wherein said polypeptide has DNA polymerase activity and 5'-3' exonuclease activity in a suitable buffer; and

b) treating said reaction mixture at a temperature and under conditions suitable for said isolated polypeptide to initiate synthesis of an extension product of said primer to provide a cDNA molecule complementary to said RNA.

It is to be understood that the skilled artisan would appreciate that the thermal cycling should be optimized to account for variations in the enzyme selected, the template to be reverse transcribed, the primers to be used to facilitate amplification (i.e., with respect to the melting and annealing temperatures), and the relative concentrations to be used for each of the reaction components. Such optimization is well within the purview of the skilled artisan; however, exemplary protocols may include the following:

Table 2 : PCR protocols

	a	b	c	d	e	# of repeated Cycles
PCR 1	94 °C, 3'	94 °C, 1'	66°C, 1'	72°C, 2'	72°C, 15'	b-d = 30
PCR 2	94°C, 3'	94 °C, 1'	62°C, 1'	72°C, 2'	72°C, 15'	b-d = 30
PCR 3	94°C, 3'	94°C, 30''	59°C, 30''	72°C, 1'	72°C, 15'	b-d = 30
PCR 4	94 °C, 3'	94 °C, 30"	68°C, 1.5'	68°C, 6'		b-c = 35
PCR 5	94 °C, 1'	94 °C, 30"	70°C, 30"	72°C, 1'	72°C, 15'	b-d = 25
PCR 6	94 °C, 3'	94 °C, 30"	59°C, 30"	72°C, 1'	72°C, 15'	b-d = 35

PCR 7	94 °C, 3'	94 °C, 1'	58 °C, 1'	72°C, 2'	72°C, 15'	b-d = 35

Moreover, it is to be understood that contemplated in the present invention is that with the polypeptide of the present invention the skilled artisan would appreciate that the buffer components and buffer concentrations should also be optimized. To this end, in a preferred embodiment, the kit of the present invention may be utilized.

As used above, the phrases "selected from the group consisting of," "chosen from," and the like include mixtures of the specified materials.

The term 'selection' relates to the parallel processing of a variants' catalytic activity (cf. affinity chromatography for the reaction product crosslinked to active phage-polymerase mutants allows the 'simultaneous' treatment of the population of phage-polymerase mutants). Selection can be achieved for a population of more than 10^7 mutants as described herein, for more than 10^{10} variants and possibly for up to 10^{14} variants. A straightforward screening of several tens of variants of the selected population enriched into active enzymes is sufficient to isolate catalysts of interest.

The term 'screening' relates to the serial processing of a variants' catalytic activity (cf. serial assays ran by a robot one well after the next one). High throughput-screening is typically done for 10^4 mutants, and generally less than 10^7 mutants.

The advantage of selection over high throughput screening is that a much larger population of mutant proteins can be analyzed for a desired catalytic activity; provided an appropriate selection strategy is available (the one described herein is one such example).

In one embodiment of a method of obtaining a thermostable variant enzyme is provided. This method comprises the following:

a) selection of enzymes expressed at the surface of phage particles and identifying at least a thermostable variant conserving its active;

catalytic domain at regulated temperature according to the method of identifying thermostable mutant polypeptides having a catalytic activity as described herein,

b) isolating and sequencing a DNA encoding said identified thermostable variant;

c) preparing a vector comprising the DNA of step (b);

d) transfecting or infecting cells with the vector obtained at step c);

e) expressing the thermostable variant enzyme from the cells and optionally,

f) recovering, isolating and purifying said thermostable variant enzyme expressed at step (e).

Where a numerical limit or range is stated herein, the endpoints are included. Also, all values and subranges within a numerical limit or range are specifically included as if explicitly written out.

The above written description of the invention provides a manner and process of making and using it such that any person skilled in this art is enabled to make and use the same, this enablement being provided in particular for the subject matter of the appended claims, which make up a part of the original description.

The above description is presented to enable a person skilled in the art to make and use the invention, and is provided in the context of a particular application and its requirements. Various modifications to the preferred embodiments will be readily apparent to those skilled in the art, and the generic principles defined herein may be applied to other embodiments and applications without departing from the spirit and scope of the invention. Thus, this invention is not intended to be limited to the embodiments shown, but is to be accorded the widest scope consistent with the principles and features disclosed herein.

Having generally described this invention, a further understanding can be obtained by reference to certain specific examples, which are provided herein for purposes of illustration only, and are not intended to be limiting unless otherwise specified.

EXAMPLES

Materials and methods

Buffers-

Buffer A (1x):

50 mM Tris-HCl at pH 8.3 at 25°C, 50 mM KCl, 10 mM $MgCl_2$, 0.5 mM spermidine, 10 mM dithiothreitol

Buffer B (1x):

20 mM Tris-HCl at pH 8.8 at 25°C, 10 mM KCl, 10 mM $(NH_4)_2SO_4$, 2 mM $MgSO_4$, 0.1% Triton X-100, 0.1 g/l BSA

Buffer C (1x):

10 mM Tris-HCl at pH 9.0 at 25°C, 50 mM KCl, 0.1% Triton X-100

Synthesis of substrates for selection-

Deoxyoligonucleotides were prepared by solid phase synthesis on a DNA synthesizer (Expedite™, Millipore). The 5'-maleimidyl derivatized primer TAA CAC GAC AAA GCG CAA GAT GTG GCG T (SEQ ID NO: 13) was synthesized as described previously (Jestin et al., 1999) purified on a C18 reverse phase HPLC column, and characterized by electrospray mass spectroscopy 8998.4 / 8999.9 (measured / calculated). 5-[-N-[N-(N-biotinyl-ε-aminocaproyl)-γ-aminobutyryl]-3-aminoallyl]-2'deoxy-uridine-5'-triphosphate (biotin-dUTP) was purchased from Sigma and the other deoxynucleotide triphosphates dATP, dCTP and dGTP were obtained from Roche-Boehringer.

Library construction-

Three phagemids libraries were mixed for phage preparation. The first two libraries (I : FseI/NotI and II : PstI/NheI) derive from mutagenic PCR amplification of the wild-type Taq gene in the presence of manganese [I: reference (Fromant, Blanquet, Plateau, 1995) with $MnCl_2$: 0.5 mM; II: reference (Cadwell, Joyce, PCR methods and amplifications, Mutagenic PCR, 3, S136-S140) with four distinct $MnCl_2$ concentrations (0.5, 0.35, 0.25 and 0.125 mM)] using following primers (I) SEQ ID NO: 1 and SEQ ID NO: 2, PCR 1, or (II) SEQ ID NO: 3 and SEQ ID NO: 4, PCR 2 (for primers: see Table 1, and for cycle settings: see Table 2).

The third phagemids library (III) was constructed by oligonucleotide assembly using the wild-type Taq gene. First, four PCR fragments were prepared using Taq polymerase (PCR 3, see Table 2), the wild-type Stoffel fragment gene as template and the following primer pairs (5-6), (7-8), (9-10) and (11-2) in buffer C 1X (for primers: see Table 1).

After purification with the QIAquick PCR Purification kit (QIAGEN), the four PCR fragments were assembled in a second PCR round using the kit GC-Advantage obtained from Clontech under PCR 4 (see Table 2), using buffer D 1X. The crude PCR product was then amplified by PCR using PCR 5 protocol, the GC-Advantage kit, and the primers 1 and 2 in buffer D 1X. Subsequently, the product was purified using the QIAquick Gel extraction gel (QIAGEN).

Buffer D 1X

40 mM Tricine-KOH (pH 9.2)

15 mM KOAc

3.5 mM $Mg(OAc)_2$

5 % DMSO

3.75 µg/ml BSA

0.005% Nonidet P-40

0.005% Tween-20

After subcloning into pHEN1 vectors using restriction sites FseI/NotI or PstI/NheI, $1.1x10^7$ distinct clones were obtained by electroporation in *E. coli* strain TG1.

Table 1 : Oligonuleotides and primers

SEQ ID NO:	Oligonucleotide sequences
1	TAACAATAGGCCGGCCACCCCTTC
2	GAGTTTTTGTTCTGCGGC
3	TTTAATCATCTGCAGTACCGGGAGCTC
4	TTCATTCTTGCTAGCTCCTGGGAGAGGC
5	CCG GCC ACC CCT TC(C AR/A VY)C TCA AC(C AR/A VY)CGG GAC CAG CTG GAA AG
6	GGA TGA GGT CCG GCA A(YT G/RB T) (YT G/RB T)AA T(YT G/RB T)GG TGC T CT TCA GCT T(YT G/RB T)GA GCT CCC GGT ACT GCA GG
7	CAA CCA GAC GGC CAC G(CA R/AV Y)AC GGG CAG GCT A(CA R/AV Y)AG CTC C(CA R/AV Y)CC CAA CCT CCA GAA CAT CC
8	CCG CCT CCC GCA C(YT G/RB T)CT TCA C(YT G/RB T)GG CCT CTA GGT CTG GCA C
9	CCT GCA GTA CCG GGA GCT C(CA R/AV Y)AA GCT GAA GAG CAC C (CA R/AV Y)AT T(CA R/AV Y)(CA R/AV Y)TT GCC GGA CCT CAT CC
10	GGA TGT TCT GGA GGT TGG G(YTG/RBT)GG AGC T(YTG/RBT)TA GCC TGC CCG T(YTG/RBT)CG TGG CCG TCT GGT TG
11	GTG CCA GAC CTA GAG GCC (CAR/AVY) GTG AAG (CAR/AVY) GTG CGG G AG GCG G
12	AAA UAC AAC AAU AAA ACG CCA CAU CUU GCG
13	TAA CAC GAC AAA GCG CAA GAT GTG GCG T
14	AAA TAC AAC AAT AAA ACG CCA CAT CTT GCG
15	TTCATTCTTGCTAGCTCCTGGGAGAGGC
16	GAG AAG ATC CTG CAG TAC CGG GAG C
17	GACCAAC ATCAAGACTGCC
18	TTGGCCAGGAACTTGTCC

Table 2: PCR cycles

	a	b	c	d	e	# of repeated Cycles
PCR 1	94 °C, 3'	94 °C, 1'	66°C, 1'	72°C, 2'	72°C, 15'	b-d = 30
PCR 2	94°C, 3'	94 °C, 1'	62°C, 1'	72°C, 2'	72°C, 15'	b-d = 30
PCR 3	94°C, 3'	94°C, 30''	59°C, 30''	72°C, 1'	72°C, 15'	b-d = 30
PCR 4	94 °C, 3'	94 °C, 30"	68°C, 1.5'	68°C, 6'		b-c = 35
PCR 5	94 °C, 1'	94 °C, 30"	70°C, 30"	72°C, 1'	72°C, 15'	b-d = 25
PCR 6	94 °C, 3'	94 °C, 30"	59°C, 30"	72°C, 1'	72°C, 15'	b-d = 35
PCR 7	94 °C, 3'	94 °C, 1'	58 °C, 1'	72°C, 2'	72°C, 15'	b-d = 35

Phage preparation and selection-

For phage preparation, *E. coli* TG1 transformed by the phagemid library and grown to an optical density of 0.3 at 600 nm were infected by a twenty-fold excess of helper phage. Phage particles were produced at 30°C for 19 hours in a 2xTY medium containing 100 mg/l ampicillin, 25 mg/l kanamycin. After removal of bacteria by two centrifugation (4000 rpm, 4°C), phage particles in the supernatant were purified by two precipitations in 4% polyethyleneglycol in 0.5 M NaCl, resuspended in 1 ml of PBS (25 mM Na_2HPO_4, 100 mM NaCl, pH 7.4), and dialyzed four times against PBS over a period of 24 hours. The pH of the final solution was raised to pH 8.

The protocol for selection was as described previously (Jestin et al., 1999), except that 10^{10} infectious phages particles were used after heating at 65°C for 5 minutes and that DNA polymerization was done at 65°C for 2 minutes.

Substrate cross-linking on phage was done by incubating the phage particles with 10 µM maleimidyl-derivatized primer, 50 µM RNA template of SEQ ID NO: 12 in the presence of 10 mM magnesium chloride at 37°C for 2 hours and polymerization during 2 minutes at 65°C after addition of 3 µM biotin-dUTP and 1 µM dVTP.

The reactions were blocked by addition of one volume of 0.25 M ethylene diamine tetra-acetate. The phage mixture was added to 300 µl of streptavidin-coated superparamagnetic beads (Dynabeads M-280, Dynal). After 30 minutes at room temperature, the beads were washed seven times and resuspended in 200 µl PBS.

The phage-bead mixture was incubated for 10 min at 37 °C after addition of one-tenth, in volume, of trypsin (0.1 g/l). 1.8 mL of *E.coli* TG1 was then added for infection during 25 min at 37 °C. Bacteria were plated on 530 cm^2 Petri dishes (Corning) with a 2xTY medium containing ampicillin (0.1 g/l). After 12 hours at 30°C, bacteria were scraped from the plates and about $2x10^9$ cells were used for preparation of the phage particles.

Variant polymerases

All variant Stoffel fragment sequences appearing in the following examples correspond to residues 13-555 of SEQ ID NO: 26, which in turn correspond to residues 290-832 of SEQ ID NO: 100, which contain one or more mutations. A summary of the mutations, the sequence designator (*e.g.*, "s," "a," "m," etc.), and the sequence identifier (*i.e.*, SEQ ID NO) appear in the Table at the end of the Examples. Each of the variants in the following examples contain a R795G mutation (i.e., residue corresponding to 518 in the sequence of SEQ ID NO: 26); however, this mutation need not be present within the context of the present invention. In other words, the present invention embraces variants corresponding to the above in which R795 is conserved. It should be noted that the only mutation appearing in variant **e** is the R795G mutation, otherwise this sequence corresponds to the wild-type Stoffel fragment (residues 13-555 of SEQ ID NO: 26).

RT-polymerization and polymerization activity assay using phage-polymerase

In the following examples, the activity of the different mutant phage-polymerases was assayed by incorporation of radiolabeled alpha ^{32}P dTTP.

Example 1 - polyclonal phage-polymerases (Figure 1):

In this example, the reverse transcriptase activity of phage-polymerases was assessed in the presence of Mg^{2+} or Mn^{2+} ions as obtained after different rounds of selection in the presence of Mg^{2+} ions. In these experiments, two reverse transcription (RT) mixes were used. The final concentration of each component in a reaction was: 10µM RNA (SEQ ID NO: 12); 5µM DNA (SEQ ID NO: 13); 0.25 mM dNTP; 3 mM $MgCl_2$ or 2.5 mM $MnCl_2$.

Each 1.9 µl aliquot of the reaction mix was further added to 15 µl of phage-polymerases (about 10^8 particles) after a given selection round heated for 5 min at 65°C. The solutions were then incubated at 37°C for 15 min. The reactions were stopped by adding 15 µl of EDTA/formamide containing denaturation solution, heating for 3 min. at 94°C, and placed on ice. The incorporation of alpha ^{32}P-dTTP was determined on 20% polyacrylamide gel; 15 µl of the final reaction volume were loaded.

The lane designations in Figure 1 are as follows:

MnCl2	$MgCl_2$
a : phage-polymerases of round 6	h: phage-polymerases of round 6
b : phage-polymerases of round 5	i : phage-polymerases of round 5
c : phage-polymerases of round 4	j : phage-polymerases of round 4
d : phage-polymerases of round 3	k : phage-polymerases of round 3
e : phage-polymerases of round 2	l : phage-polymerases of round 2
f : phage-polymerases of round 1	m : phage-polymerases of round 1
g : phage-polymerases of initial population	n : phage-polymerases of initial population

This experiment demonstrated that:

- A RT-activity is present using phage-polymerase obtained after round 5 (i) or 6 (h) of selection in presence of Mg^{2+}.
- A high RT-activity was detected at the round 3 (d) in the presence of Mn^{2+} and for further rounds.

Example 2 - polyclonal phage-polymerases (Figure 2):

In this example, the reverse transcriptase activity of phage-polymerases was assessed as obtained after different rounds of selection in the presence of Mg^{2+} ions. In these experiments, a reverse transcription (RT) mix was used. The final concentration of each component in a reaction was: 10µM RNA (SEQ ID NO: 12); 5µM DNA (SEQ ID NO: 13); 0.25mM dNTP; 3mM $MgCl_2$.

Each 1.2 µl aliquot of the reaction mix was further mixed with 15 µl of phage-polymerase polymerases (about 10^8 particles) after one round of selection round, either not preheated or heated 5 min at 65°C before reaction of polymerization. The solutions were then incubated at 37°C for 15 min. The reactions were stopped by adding 15 µl of the denaturation solution, heating for 3 min. at 94°C and placing on ice.

The incorporation of alpha ^{32}P-dTTP was determined on 20% polyacrylamide gel; 15 µl of the final reaction volume were loaded. The positive control was performed with addition of different concentration of commercial AMV reverse transcriptase (Promega).

The lane designations in Figure 2 are as follows:

Phage-polymerase preheated at 65 °C for 5 min.	Phage-polymerase not preheated
a : phage-polymerases of initial population	h : phage-polymerases of initial population
b : phage-polymerases of round 1	i : phage-polymerases of round 1
c : phage-polymerases of round 2	j : phage-polymerases of round 2
d : phage-polymerases of round 3	k : phage-polymerases of round 3
e : phage-polymerases of round 4	l : phage-polymerases of round 4
f : phage-polymerases of round 5	m : phage-polymerases of round 5
g : phage-polymerases of round 6	n : phage-polymerases of round 6
	o : control AMV-RT, 1 U
	p : control AMV-RT, 0.1 U
	q : control AMV-RT, 0.01 U
	r : control AMV-RT, 0.001 U

This experiment demonstrated that:

- A RT-activity is present using phage-polymerase obtained after round 5 or 6 of selection preheated for 5 min. at 65°C (f and g) or not (m and n) as in Figure 1 in presence of Mg^{2+}.
- A high RT-activity was detected using 1 unit of AMV-RT (o) but no activity was detected using decreasing concentration of AMV-RT.

Example 3 - monoclonal phage-polymerases (Figure 3):

In this example, the reverse transcriptase activity of various monoclonal phage-polymerases obtained after round 6 in the presence of Mg^{2+} ions was assessed. In these experiments, a reverse transcription (RT) mix was prepared in which the final concentration of each component in a reaction was: 10µM RNA (SEQ ID NO: 12); 5µM DNA (SEQ ID NO: 13); 0.25mM dNTP; 3 mM $MgCl_2$.

Each 1.45 µl aliquot of the reaction mix was further mixed with 15 µl of phage-polymerase heated for 5 min at 65°C. The solutions were then incubated at 37°C for 20 min. The reactions were stopped by adding 15 µl of denaturation solution, heating for 3 min. at 94°C, and placed on ice.

The incorporation of alpha ^{32}P-dTTP was determined on a 20% polyacrylamide gel; 15 µl of the final reaction volume were loaded. The positive control was performed using the AMV-RT (Promega), lane C.

The different monoclonal phage-polymerases were obtained among the phage-polymerases of round 6. The phage-polymerases present various DNA-polymerase RNA-dependant activities. The lane designations in Figure 3 are as follows: s = SEQ ID NO: 38; a = SEQ ID NO: 20; d = SEQ ID NO: 24; g = SEQ ID NO: 28; C = AMV-RT; i = SEQ ID NO: 30; m = SEQ ID NO: 32; n = SEQ ID NO: 34; b = SEQ ID NO: 22; and q = SEQ ID NO: 36.

The clones **a**, **b**, and **d** possess a high RT-activity, which were further studied as reported in Figure 4. Randomly chosen clones from the selected populations were assayed for monoclonal phage-polymerase reverse transcriptase activity and that further sequencing of the corresponding mutant genes revealed identical sequences (for example, 7 clones reported in the figure were found to have the same sequence noted **a**).

Example 4 - monoclonal phage-polymerases (Figure 4):

In this example, the reverse transcriptase and the polymerase activities of monoclonal phage-polymerases obtained after the round 6 in the presence of Mg^{2+} or Mn^{2+} ions was assessed. In these experiments, the final concentration of each component in a reaction was:

10µM RNA (SEQ ID NO: 12); 5µM DNA (SEQ ID NO: 13); 0.25mM dNTP; 3 mM $MgCl_2$ or 2.5 mM $MnCl_2$; and

1µM DNA (SEQ ID NO: 14); 1µM DNA (SEQ ID NO: 13); 0.25mM dNTP; 3 mM $MgCl_2$ or 2.5 mM $MnCl_2$;

2 µl aliquots of the reaction mix were further added to 15 µl of each phage-polymerase pre-heated for 5 min at 65°C. The solutions were then incubated at 37°C for 15 min. The reactions were stopped by adding 15 µl of denaturation solution, heating 3 min. at 94°C, and placed on ice.

The incorporation of alpha ^{32}P-dTTP was determined on polyacrylamide gel; 15 µl of the final reaction volume were loaded. The positive control was performed using the phage Stoffel fragment (**e**).

The lane designations in Figure 4 are as follows: a = SEQ ID NO: 20; b = SEQ ID NO: 22; d = SEQ ID NO: 24; and e = SEQ ID NO: 26 (containing an R518G mutation).

Three families of phage polymerase were characterized among the phage-polymerases of round 6.

- The phage-polymerases **a** and **b** present a high DNA-polymerase DNA-dependent activity, which is higher than that of Stoffel phage-polymerase.
- The phage-polymerases **b** and **d** present a high DNA-polymerase RNA-dependent activity, which is higher than that of the Stoffel phage–polymerase **e** (not detectable, see Figure 4) or than the phage-polymerase **a**, whatever the conditions in the presence of magnesium or of manganese.
- The phage-polymerase **d** shows a poor DNA-polymerase DNA-dependent activity, which is lower than the activity of the Stoffel phage–polymerase.

Construction and overproducing clones-

Three phagemids corresponding to clones **a**, **b** and **d** on Figure 4 were isolated from individual colonies of *E. coli* strain TG1. The plasmid DNA was prepared and purified using Wizard Plus miniprep kits. The phagemids were cleaved with NcoI and NotI restriction endonucleases and the fragments ligated into an expression vector deriving from pET-28b(+) (Novagen) that had been cleaved with NcoI and NotI and dephosphorylated with alkaline phosphatase. This pET vector contains a sequence for the thrombin cleavage site between the NotI and XhoI restriction sites of pET 28b(+) (GCGGCCGCACTGGTGCCGCGCGGCAGCCTCGAG; SEQ ID NO: 45).

Recombinant plasmids were transformed in *E. coli* strain BL21(DE3) pLysS and plated on 2YT media with kanamycin and chloramphenicol. Correct plasmid constructions were initially identified by restriction analysis of plasmid miniprep.

E. coli strain BL21(DE3) pLysS, used as a host for recombinant plasmids to over produce the mutant polymerase, was grown in 2YT medium supplemented with 10 µg/ml kanamycin and 25 µg/ml chloramphenicol to propagate plasmids. At an optical density of 0.6 at 600 nm, 1 mM of isopropyl-1-thio-β-D-galactopyranoside (IPTG) was added to induce production of enzyme for 5 hours.

Purification of mutant polymerases-

Mutants were prepared from 500 ml batches of cells. 2YT media plus kanamycin and chloramphenicol was inoculated with bacteria (containing a recombinant plasmid) freshly picked on a plate and grown at 37 °C to an absorbance at 600nm of approximately 0.5. Subsequently, IPTG was added to a final concentration of 1 mM and the cultures were allowed to further grow for 5 h.

Cells were harvested by centrifugation at 15000 g and 4°C for 10 min., resuspended in 30 ml of lysis buffer (50 mM Na_2HPO_4, 300 mM NaCl, 5 mM imidazole, pH= 8), lysed 3 times for 45 sec by ultrasound. Cell debris were removed by centrifugation at 10000 g and 4°C for 15 min.

Mutant polymerases were recovered from this clarified lysate and purified using Ni-NTA agarose (QIAGEN).

Example 5 - Purified mutant polymerases **a**, **b**, and **d** used in RT-polymerase chain reaction (Figure 5):

The positive control was performed using the polymerase AMV-RT (Promega). These studies were performed using the three clones corresponding on clones **a**, **b** and **d** in Figure 4.

The reverse transcription was performed at 65°C during 1 h using the following conditions.

Control RT mix

Component	Amount
RNA from rabbit globin (sigma), 20 µg/ml	1 µl
primer 17 (5 µM)	0.4 µl
primer 18 (5 µM)	0.4 µl
buffer A (**)AMV-RT 5X	3 µl
dNTP 2.5 mM	0.8 µl
AMV-RT 10 U/µl	3 µl
water	6.4 µl

(**) See buffer A composition above

RT mix

Component	Amount
RNA from rabbit globin (sigma), 20 µg/ml	1 µl
primer 17 (5 µM)	0.4 µl
primer 18 (5 µM)	0.4 µl
$MgCl_2$ 25 mM	0.75
buffer C (***)	1.5 µl
dNTP 2.5 mM	0.8 µl
mutant polymerase **a**, **b**, **d**	3 µl
or the Stoffel fragment **e**	
water	7.15 µl

(***) See buffer C composition above

The PCR was performed using PCR 7 (see table 2) and following conditions.

PCR mix

Component	Amount
Buffer B 10x	20 µl
primer 17 (50 µM)	4 µl
primer 18 (50 µM)	4 µl
dNTP	2 µl
water	164.5 µl
Taq DNA polymerase (5U/µl)	5 µl
Pfu polymerase (3U/µl)	0.5 µl

19 µl aliquot of the PCR mix was added to 1 µl of the RT reaction product.

A RT-PCR product of 372 bp was detectable using mutant polymerases **b** and **d**.

The lanes in the gel appearing in Figure 5 include the three clones corresponding to clones **a**, **b** and **d** on Figure 4. In addition, the positive control was performed using the Stoffel fragment polymerase **e** and the commercial AMV-RT (Promega).

The lanes in Figure 5 are as follows:

lane 1 : molecular weight marker: PhiX phage DNA digested by *Hae*III.

lane 2 : control AMV-RT

lane 3 : b = SEQ ID NO: 22

lane 4 : a = SEQ ID NO: 20

lane 5: e = SEQ ID NO: 26 (containing an R518G mutation)

lane 6 : d = SEQ ID NO: 24

Example 6 - Optimization of the production and of the purification of the polymerases.

Variant polymerases were expressed in *Escherichia coli* strain BL21(DE3) pLysS using a pET vector. The inventors improved the yield and the reproducibility of production of these proteins by (a) a chemical lysis of the cells and (b) a pre-purification by heating at 80°C for 10 or 15 minutes (denaturation, elimination by precipitation and centrifugation of the proteins thermically unstable).

The optimization of the two steps (a) and (b) allows a more effective purification of variants by chromatography.

After affinity chromatography by using the six histidine tag, inventors obtained, starting from about 1.2 to 1.6 liters of culture, until about 0.1 to 0.3 mg of protein of purity, estimated on polyacrylamide gel, comprised between 80% and 90%

Further purification steps were done prior to kinetic studies (see Example 10).

Protocol Of Production And Purification Of Proteins:

Production of variants **d**, **b**, **a** and **e**.

- Electroporation of 50 µl of electro-competent cells BL21(DE3) pLysS by the expression pET plasmid containing mutated or wild-type genes (e, fragment of Stoffel of the Taq polymerase) coding for the proteins polymerases to be produced.
- Incubation 1 hour at 37°C in 3 ml of 2YT medium under agitation.
- Spreading out with beads of 100 and 200 µl per Petri dish containing 2YT agarose with kanamycin (10µg/ml) and chloramphenicol (30µg/ml).
- Incubation at 37°C for 16 hours.
- The colonies are recovered and suspended in 400 ml of 2YT medium with kanamycin (10µg/ml) and chloramphenicol (30µg/ml).

- Incubation at 37°C of the culture until the OD at 600 nm is about 0.6.
- Induction of the expression of the proteins by addition of IPTG (1mM final concentration).
- Incubation about 16 hours at 37°C under agitation.
- Centrifugation of the cultures at 8000 rpm, 10 min., 4°C.

Purification

- The pellets were treated by 45 ml of BugBuster (BugBuster Protein Extraction Reagent-NOVAGEN, Ref. 70584).
- Incubation at room temperature under agitation 20 - 40 min.
- Centrifugation at 10000 rpm, 10 min., 21°C.
- Supernatants were recovered and treated 10 min. at 80°C under agitation prior to colling at 4°C
- Centrifugation at10000 rpm, 10 min., 4°C.

Capture of the proteins by affinity chromatography for the His tag

The Talon Metal Affinity Resin (2ml., Clontech) was washed twice with the buffer BBW (50 mM sodium phosphates, 300 mM NaCl, pH=7) prior to incubation for 30 minutes at 4°C with the supernatant.

After three washing steps with the BBW buffer (20 ml.), the proteins were eluted from the resin.

Elution

Add to each resin pellet to be eluted, 2 ml of 1X Elution Buffer: Imidazole Elution (pH7, 50 mM Sodium Phosphates, 300 mM NaCl, 150 mM Imidazole).

- **FRACTION 1:** Homogenize 10 min. with at cold temperature and centrifuge 700g, 3min., 4°C. Recover the supernatant (2ml). Add 2ml 1X Elution Buffer, Homogenize 5min.
- **FRACTION 2**: Centrifuge 700g, 3min., 4°C. Recover supernatant (2ml). Add 2ml 1X Elution Buffer, Homogenize 5min.
- **FRACTION 3**: Centrifuge 700g, 3min., 4°C. Recover supernatant (2ml).

Preserve an aliquot of some µl of each fraction, at 4°C, for its migration on 10% Acrylamide Gel.

Concentration and elimination of proteins of small molecular weight.

- Pool the three fractions = 4-5ml and chromatography them on Ultra-4 column AMICON, 50000NMWL, (Amicon Ultra centrifugal filter devices with low-binding Ultracel membrane - MILLIPORE, Ref. UFC8 050 24).
- Centrifuge 15 min., 3000g, 25°C.
- Washing and/or change buffer by addition to the column of 4 ml of 100 mM Tris pH 8 buffer.
- Centrifuge 15min., 3000g, 25°C.
- Obtaining of 30µl of each purified and concentrated protein.
- Addition of 270µl of storage buffer [50 mM Tris HCl pH8; 100 mM NaCl; 0,1 mM EDTA; 1mM DTT] (final volume = 300µl)
- The concentrated and purified proteins are stored at 4°C.
- The purity and the concentration of the purified polymerases are evaluated by SDS PAGE.

Protein dosage is carried out on 1/10 diluted samples in Tris 100mM pH 8 buffer, with the BioPhotometer 6131 (Eppendorf)

Purification Control

Polyacrylamide gels were stained with Coomassie Blue (see Figures 6 and 7);

M is the SDS PAGE molecular weight standards. Low Range (BIO-RAD, Ref. 161-0304). Bands at 97.4 kDa; 66.2 kDa; 45 kDa; 31 kDa; 21 kDa and 14.4 kDa.

Catalytic Properties Of The Polymerases:

Example 7 - Primer extension:

The three variants of interest (proteins with the histidine tag) were used in a primer extension assay using radiolabelled primers. These variants have a strong DNA-dependent DNA-polymerase activity at 65°C. For two of them (**b** and **a**) this activity

was almost the same as that of the fragment of Stoffel (**e**) produced and purified under the same conditions (see Figure 8: Gel 1).

On the other hand, reverse transcriptase activity detected at 65°C for both variants **d** and **b** (respectively **a**) is much higher than the reverse transcriptase activity obtained in the presence of magnesium for the fragment **e** (see Figure 8: Gel 2).

The present inventors also checked the thermal stability of these variants. The DNA-dependent DNA-polymerase activity was maintained after an incubation of proteins 45 min. at 65°C. This maintenance of the catalytic activity DNA-dependent DNA-polymerase on variants was necessary for the design of a protocol of "RT-PCR one-pot".

The inventors confirm that the method of the present invention should allow the acquisition of polymerase variants having the catalytic activities required for such of "RT-PCR one-pot" protocol. One embodiment is given in Example 9.

Products of primer extension with polymerases e, a, d and b:

DNA polymerases **e**, **a**, **b** and **d** were prepared and further purified using the six-histidines tag as described in the paragraph before Example 6.

Materials:

A mixture consisting of 1 µl of variant histidine tagged enzymes **e** (960 mg/l), **a** (870 mg/l), **b** (910 mg/l) and **d** (510 mg/l), template (the oligoribonucleotide of SEQ ID NO: 12 or the deoxyribonucleotide of SEQ ID NO: 14), DNA primer 13 (SEQ ID NO: 13), 0.25 mM dNTP, 3 mM $MgCl_2$ in buffer B 1x was incubated at 65°C for 5 minutes. After denaturation at 94°C, the samples were loaded on a 20% polyacrylamide gel for electrophoresis.

Method:

GEL 1: 1 µl of the concentrated fraction of each variant is added to 15 µl of the reaction mixture [0.5 µM DNA template (AAATACAACAATAAAACGCCACATCTTGCG; SEQ ID NO 14); 0.5 µM DNA (TAACACGACAAAGCGCAAGATGTGGCGT; SEQ ID NO: 13); 0.25 mM dNTP; 3 mM $MgCl_2$; 1X buffer C].

- Polymerization is carried out at 65°C during 5 min.
- The reaction is stopped by addition of 15 µl of solution of denaturation, heated at 94°C and then placed at 4°C.
- 15 µl of each sample are deposited onto the gel.

GEL 2: 1 µl of the concentrated fraction of each variant is added to 15 µl of the reaction mixture [10 µM RNA (AAAUACAACAAUAAAACGCCACAUCUUGCG; SEQ ID NO: 12); 5 µM DNA (TAACACGACAAAGCGCAAGATGTGGCGT; SEQ ID NO: 13); 0,25 mM dNTP; 3 mM $MgCl_2$, 1X buffer C].

- Polymerization is carried out at 65°C during 5 min.
- The reaction is stopped by addition of 15 µl of solution of denaturation, heated at 94°C and then is placed at 4°C.
- 15 µl of each sample are deposited on each gel.

The results for gels 1 and 2 are shown in Figure 8.

Example 8 - Optimization of PCR:

The present inventors have developed a PCR protocol for the amplification of DNA fragments. The hybridization of the primers to the template and the polymerization are carried out at 65°C. The PCR reaction of a DNA template by variants **a** and **e** were tested. Materials and methods are described below and results are shown in Figure 9.

Furthermore, the PCR reaction of a DNA template by variant **a,** for which kinetic analysis was made, was tested on two different thermocyclers (MJ Research and Applied Biosystems), the results obtained with these machines are comparable for the amplification of a fragment of about 450 bp (see Figure 9). This result was extended to the amplification of a fragment of about 1560 bp (see Figure 10).

Briefly, the catalytic properties of variant **a** evaluated by PCR are very similar to those of the Stoffel fragment of the Taq polymerase (**e**).

Products of PCR with polymerase e and variant a (Figure 9):

PCR Reaction mixture (for 20 µl) :

Variants **a** and **e** (purified and diluted 1/10 in Tris 100mM)	1.5µl
Thermophilic DNA Polymerase 10 X	
buffer, Magnesium Free, Promega	2µl
Primer 1 fwd (100µM)	0.125µl
Primer 2 rev (100µM)	0.125µl
dNTP at 25mM	0.2µl
DNA template (pGL2-luciferase, 10 ng)	1µl
$MgCl_2$ (25mM)	1µl
H_2O	9.05ml

Temperature Cycle on PTC-100 (MJ RESEARCH)

94°C, 1min. ; [94°C, 20 sec ; 65°C, 4min]$_{40\ cycles}$; 65°C, 15min.

Sequences of the primers

Primer 1 fwd : GGA TGG AAC CGC TGG AGA GCA ACT G (SEQ ID NO: 101)

Primer 2 rev : GAT CTC TCT GAT TTT TCT TGC GTC G (SEQ ID NO: 102)

In a 20 µl reaction volume, 1.5µl of polymerases **e** (960 mg/l) or **a** (870 mg/l) were mixed with 10 ng of template (plasmid pGL2-luciferase, Promega), 0.6 µM primer 111 (GGA TGG AAC CGC TGG AGA GCA ACT G; SEQ ID NO: 101), 0.6 µM primer 112 (GAT CTC TCT GAT TTT TCT TGC GTC G; SEQ IND NO: 102)), 0.25 mM dNTP, 2.5 mM $MgCl_2$ in buffer B 1x prior to incubation at the following temperature/time steps (94°C/1min.) (94°C/20 sec; 65°C/4min)$_{40\ cycles}$ (65°C/15min.)on a PTC100 thermocycler (MJ Research) to yield an about 1560 bp long PCR product as shown on the figure representing the agarose gel after electrophoresis. M is the marker Smartladder (Eurogentec).

Variant **a** : obtaining a fragment of 475bp (Figure 10)

Reaction mixture for PCR (for 20 µl of reaction)

Variant a	**1.5 µl**
Thermophilic DNA Polymerase 10 X buffer, Magnesium Free, Promega	2 µl
Primer 1 Fwd (50µM)	0.5 µl
Primer 2 Rev (50uM)	0.5 µl
dNTP set (25mM)	0.2 µl
$MgCl_2$ (25mM)	1µl
DNA template (pHEN1-Taq, about 10 ng)	1µl
H_2O	13.3µl

Temperature cycles on PTC -100 (MJ RESEARCH)

94°C, 1min.; [94°C, 20 s; 65°C, 4min]35 cycles; 65°C, 15min.

Temperature cycles on GeneAmp PCR System-9700 (Applied BioSystems)

94°C, 1min.; [94°C, 20 s; 66,5°C, 4min]40 cycles; 65°C, 15min.

Sequences of the primers

Primer 1 fwd: GAG AAG ATC CTG CAG TAC CGG GAG C (SEQ ID NO: 16)

Primer 2 rev: TTC ATT CTT GCT AGC TCC TGG GAG AGG C (SEQ ID NO: 4)

RT-PCR

Subsequent to optimisation of the temperature cycles, the buffer and the additives used, the present inventors realized a reaction of "RT-PCR one-pot" with variant **a** without addition of reagents after the beginning of the reaction (Example 9 and Figure 11). This result was been reproduced for two distinct buffers containing magnesium ions (without manganese ions) on two different thermocyclers with the same batch from RNA (rabbit globin mRNA, Sigma R1253) and the same batch of variant **a**.

The present inventors tested this RNA in a "RT-PCR one-pot" reaction using the commercial kit of Applied Biosystems (Gene Amp AccuRT RNA PCR). The RNA is amplified in the form of a slightly visible band.

Example 9 - RT-PCR "one pot" (Figure 11):

Reaction mixture of RT-PCR "one-pot" (or 25 µl of reaction)

Variant a	1 µl (column 5) ; 0.5 (column 4)
Thermophilic DNA Polymerase 10 X buffer, Magnesium Free, Promega	2.5 µl
Primer 1 fwd (50µM)	0.25 µl
Primer 2 rev (50µM)	0.25 µl
dNTP set (25mM)	0.25 µl
$MgCl_2$ (25mM)	0.75 µl
mRNA globin SIGMA (20 ng/µl)	0.25 µl
Adjuvant 1	1 µl
Adjuvant 2	0.4 µl
H_2O	18.35 µl

Cycle temperature on PTC-100 (MJ RESEARCH)

94°C, 15 s.; 65°C, 45 min.; [94°C, 20 s; 65°C, 4min]$_{32\ cycles}$; 65°C, 15min.

Sequences of the primers:

Primer 1 fwd: TTG GCC AGG AAC TTG TCC (SEQ ID NO: 18)

Primer 2 rev: GAC CAA CAT CAA GAC TGC C (SEQ ID NO: 17)

Amplification product = 372 bp.

In a 25 µl reaction volume, 0.5 or 1 ml of purified and six histidines-tagged polymerase **a** (117 mg/l) were mixed with 5 ng of template (rabbit globin messenger RNA, Sigma), 0.5 µM primer 113 (GAC CAA CAT CAA GAC TGC C; SEQ ID NO: 17), 0.5 µM primer 114 (TTG GCC AGG AAC TTG TCC (SEQ ID NO: 18), 0.25 mM

dNTP in a manganese-free buffer B 1x containing 1.25 mM $MgCl_2$, 1 mg acetamide and 8 µM tetramethyl ammonium chloride, prior to incubation at the following temperature/time steps (94°C/15 s; 65°C/45 min.)(94°C/30 s; 65°C/4min)$_{32\ cycles}$ (65°C,15min.) on a thermocycler (Biometra) to yield an about 372 bp long PCR product as shown in Figure 11 representing the agarose gel after electrophoresis. M is the marker of phage PhiX DNA digested by the restriction enzyme *Hae*III.

Example 10 – Kinetic parameters for variant a:

For evaluation of the kinetic parameters, polymerase **a** after purification by affinity chromatography for the histidine tag was cleaved at 23°C by the protease thrombin for release of the tag and further purified on a heparin column (Pharmacia) prior to characterisation by SELDI TOF mass spectrometry. Remaining His-tagged polymerases were finally removed by incubation with Co^{2+} resin (Talon Metal Affinity resin).

k_{cat}	$0.1\ s^{-1}$
K_m(dNTP)	3.10^{-5} mol l^{-1}
k_{cat} / K_m(dNTP)	3.10^{3} l.mol^{-1}.s^{-1}

for the RNA templates (AAG CCU ACG ACU CCG AAC UGA CCG UGC UAC CAA U; SEQ ID NO: 103), (AAG CCU ACU ACU CCG AAC UGA CCG UGC UAC CAA U; SEQ ID NO: 104), (AAG CCU ACA ACU CCG AAC UGA CCG UGC UAC CAA U; SEQ ID NO: 105) and for the primer DNA (A TTG GTA GCA CGG TCA GTT CGG AGT ; SEQ ID NO: 106) and for dNTPs (N=A, C or T).

The catalytic efficiency for RNA-dependent DNA-polymerisation measured as k_{cat} / K_m(dNTP) is about ten fold higher for variant **a** than variant **e**.

Example 11 – Identification of new variants:

96 clones were isolated starting from the population selected from phage-polymerases after the sixth cycle from evolution directed towards the reverse transcriptase activity. 91 genes coding for the variant of polymerase were sequenced and characterized. 19 additional and distinct sequences to those described in the

examples above, labelled "rtX" appearing in the table below, were identified. The corresponding phages-polymerases were prepared as previously described. The catalytic activities of the phage-polymerases were controlled by primer extension by using radio-labelled primers. In these assays for phage-polymerases, some variants have a whole DNA-dependent - DNA-polymerase activity at 65°C. In these assays, some variants seem to have a very strong RNA-dependent DNA-polymerase activity at 65°C. The results for this study are shown in Figure 12.

These results will enable the inventors to establish a link between the sequence and the catalytic activity of the phages-polymerases selected. These data support a utility in "RT-PCR one-pot".

Summary of the Taq Sequence Variants above-

In the N-terminus of the purified proteins, the signal sequence appearing in SEQ ID NOs: 19-38 (polynucleotide sequence – odd numbered sequences, protein sequence - even numbered sequences) is not taken in account, i.e., the peptide having the sequence $MASG_4CG_4$ (SEQ ID NO: 39), which has been introduced upstream of the sequence SPKA (amino acids 13-16 of SEQ ID NO: 26). The latter sequence corresponds to the Stoffel fragment beginning (S being the amino acid occupying the position number 290 in the Taq polymerase sequence).

In the C-terminus of the purified proteins, the sequence $AAALVPRGSLEH_6$ (SEQ ID NO: 40) comprising a site of cleavage by thrombin appearing in SEQ ID NOs: 19-38 (polynucleotide sequence – odd numbered sequences, protein sequence - even numbered sequences), as well as a polyhistidine tag that was introduced to facilitate further purification of the protein are also not taken into account or are not essential for the sequences of the present invention.

Further, the C-terminal alanine dipeptide appearing in SEQ ID NOs: 62-99 (polynucleotide sequence – even numbered sequences, protein sequence - odd numbered sequences) can similarly be removed to obtain the sequences of the present invention.

Clearly, the present invention contemplates and embraces sequences that have been modified to contain one or more of the following: a N-terminal leader/signal sequence, an N-terminal fusion, the remainder of the N-terminal region (residues 1-200)

of the Taq polymerase wild-type sequence SEQ ID NO: 100, a C-terminal cap resulting from protease cleavage (e.g., thrombin), a C-terminal fusion, a C-terminal purification tag, etc.

In a particularly preferred embodiment of the present invention are the following variants of the Taq polymerase. More particularly preferred are the variants represented by residues 13-555 of SEQ ID NOs: 20, 22, 24, 28, 30, 32, 34, 36, and 38, and the variants represented by residues 1-543 of SEQ ID NOs: 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, and 98.

Mutations assessment[1,2]	sequence	SEQ ID NO:
M761V	"s"	38
M761T, D547G, I584V	"a"	20
W827R	"m"	32
W827R, E520G, A608T	"b"	22
W827R, A517V, T664S, F769S	"g"	28
M747K, Q698L, P816L	"n"	34
M747R, W604R, S612N, V730L, R736Q, S739N, N483Q, S486Q, T539N, Y545Q, D547T, P548Q, A570Q, D578Q, A597T	"d"	24
F749Y, A568V	"i"	30
F749Y, P550Q, R556S, V740E, V819A	"q"	36
Stoffel Fragment (e)[3]	"e"	26
E530G, Y696C, A803V	"rt1"	63
H480R, W827R	"rt2"	65
V586I, I638F, M747K, G776E	"rt3"	67
T509S, L552H, M779K	"rt16"	69
Q534R, A764T	"rt18"	71
F482L, T664A, F749Y, P770T, M775T	"rt25"	73
L552P, A661T, A800V, E820K	"rt26"	75
I553F, A608V, F749S	"rt28"	77
E742K, M747K	"rt30"	79
M747R	"rt31"	81
A608V	"rt33"	83
R651Q	"rt36"	85
M747K	"rt43"	87
Y696N	"rt59"	89

Y696C	"rt64"	91
I599N, L780P, E820K	"rt70"	93
Y696C, K767E	"rt78"	95
D551G, V783I	"rt80"	97
S612N, P816S	"rt86"	99

[1] Amino acid numbers correspond to position in the Taq polymerase wild-type sequence SEQ ID NO: 100.

[2] All sequences contain a R795G mutation (i.e., residue corresponding to 518 in the sequence of SEQ ID NO: 26); however, this mutation need not be present within the context of the present invention. In other words, the present invention embraces variants corresponding to the above in which R795 is conserved.

[3] Wild-type Stoffel fragment (residues 13-555 of SEQ ID NO: 26) listed for reference purposes; however, as stated herein above, variant e also contains a R795G mutation, which is not reflected in SEQ ID NO: 26 appearing in the Sequence Listing.

Numerous modifications and variations on the present invention are possible in light of the above teachings. It is, therefore, to be understood that within the scope of the accompanying claims, the invention may be practiced otherwise than as specifically described herein.

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